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Subject:

Jiang, Dong  
Tuesday, March 11, 2003 6:40 PM  
STIC-Biotech/ChemLib  
09/636,530

88794  
Priority = ED = 8/10/00  
Cantor, T.

Please search SEQ ID NO:2 and 3

-issued & publ.  
-commercial

Please send results on paper to Dong Jiang in 10D-08 (mail stop CM1-10D19).  
Thank you very much.

Dong Jiang (78243)  
703-305-1345  
U.S. Patent and Trademark Office  
Art Unit 1646  
dong.jiang@uspto.gov  
CM1-10D08  
Mail stop: CM1-10D19

RECEIVED  
MAR 12 2003  
(STIC)  
Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 3/13/03  
Date Completed: 3/19/03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: 2  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: EDP  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

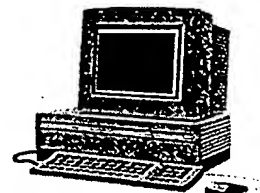
**THIS PAGE BLANK (USPTO)**



# BioTech-Chem Library

## Search Results

### Feedback Form (Optional)



Scientific & Technical Information C

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4:  
CM-1 Room 1E01

---

#### *Voluntary Results Feedback Form*

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

*Types of relevant prior art found:*

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

**Other Comments:**

---

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or [mary.hale@uspto.gov](mailto:mary.hale@uspto.gov)

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KW bone formation; osteoporosis; hypoparathyroidism; hypertension;  
 KW climacteric disturbance.  
 XX  
 OS Synthetic.  
 XX  
 PN EP748817-A2.  
 XX  
 PD 18-DEC-1996.  
 XX  
 PF 13-JUN-1996: 96EP-0109475.  
 XX  
 PR 15-JUN-1995: 95JP-0148652.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Fukuda T, Hatabshita J, Nakagawa S, Takeomi S;  
 DR WPI; 1997-036114/04.  
 XX  
 PT New parathyroid hormone derivs. - useful in treatment of bone  
 PT diseases, hypoparathyroidism and hypertension  
 XX  
 PS Claim 3; Page 39; 42pp; English.  
 XX  
 CC The sequences given in AAM08103-07 represent fragments of human para-  
 CC thyroid hormone (PTH) which were used as Xaa34-4q the generic sequence  
 CC given in AAM08102. Peptides based on the generic sequence are human PTH  
 CC (1-34) derivative peptides. They have potent CAMP-producing activity and  
 CC bone formation activity. They may be used in treatment of bone  
 CC diseases including osteoporosis, hypoparathyroidism, hypertension  
 CC and climacteric disturbance. The peptides are low in toxicity and  
 CC are safe.  
 XX  
 SQ Sequence 51 AA:  
 XX  
 QY Query Match 98.0%; Score 248; DB 18; Length 51;  
 Best Local Similarity 98.0%; Pred. No. 3, 8e-26;  
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEADKADVNLTKAKSQ 51  
 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEADKADVNLTKAKSQ 51  
 RESULT 5  
 AAR11732  
 ID AAR11732 standard; Protein; 55 AA.  
 XX  
 AC AAR11732;  
 XX  
 DT 03-JUL-1991 (first entry)  
 XX  
 DE PTH-(29-84).  
 XX  
 KW Parathyroid hormone; calcium; osteoporosis; bone.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9105050-A.  
 XX  
 PD 18-APR-1991.  
 XX  
 PF 01-OCT-1990: 90WO-C000335.  
 XX  
 PR 29-SEP-1989: 89CA-2615001.  
 XX  
 PA (CANA ) NAT RES COUNCIL CAN.  
 XX  
 PI Sung WL;  
 DR WPI; 1991-132857/18.  
 DR N-PSDB; AA011618.  
 XX

PT Mature human parathyroid synthesis - inclides using eg E. coli  
 PT transformed by plasmid contg. synthetic nucleotide sequence contg.  
 PT adenine rich codons in N-terminal region.  
 XX  
 PS Disclosure; Fig 6; 62pp; English.  
 XX  
 CC Codons 29-84 are degenerate in the usage frequency favoured by  
 CC E.coli or yeast. Codons 1-28 (see AA011617) are designed to contain  
 CC adenine rich codons. The sequence is prepd. from eight oligo-  
 CC nucleotides (4 on each strand). A plasmid contg. the complete  
 CC sequence expresses PTH with an improved yield. PTH is a blood  
 CC calcium regulator known to increase bone mass.  
 XX  
 SQ Sequence 55 AA:  
 XX  
 QY Query Match 98.0%; Score 248; DB 12; Length 55;  
 Best Local Similarity 98.0%; Pred. No. 4, 2e-26;  
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 DB 5 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEADKADVNLTKAKSQ 55  
 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEADKADVNLTKAKSQ 51  
 5 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEADKADVNLTKAKSQ 55  
 RESULT 6  
 AAR30852  
 ID AAR30852 standard; Protein; 78 AA.  
 XX  
 AC AAR30852;  
 XX  
 DT 09-JUN-1993 (first entry)  
 XX  
 DE hPTH mutetin lacking 6 N-terminal amino acids.  
 XX  
 KW Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;  
 KW hypercalcaemia.  
 XX  
 OS Synthetic.  
 XX  
 PN EP528271-A.  
 XX  
 PD 24-FEB-1993.  
 XX  
 PF 05-AUG-1992: 92EP-0113322.  
 XX  
 PR 07-AUG-1991: 91JP-0198056.  
 XX  
 PR 26-JUN-1992: 92JP-0169713.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Fukuda T;  
 DR WPI; 1993-060187/08.  
 DR N-PSDB; AA035228.  
 XX  
 PT New human parathyroid mutetin(s) - useful for treating e.g.  
 PT osteoporosis, hypoparathyroidism, hyperparathyroidism,  
 PT hypercalcaemia, hypertension etc.  
 XX  
 PS Disclosure; Page 7; 88pp; English.  
 XX  
 CC The sequence is that of a human parathyroid hormone (hPTH) peptide  
 CC lacking 6 hPTH N-terminal amino acids. The peptide can have higher  
 CC stability, enhanced activity and improved absorption by tissues.  
 CC It can act as a PTH antagonist and can be used as a therapeutic  
 CC agent for hypercalcaemia and hyperparathyroidism.  
 XX  
 SQ Sequence 78 AA:  
 XX  
 QY Query Match 98.0%; Score 248; DB 14; Length 78;  
 Best Local Similarity 98.0%; Pred. No. 6, 5e-26;  
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
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 DB 28 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEADKADVNLTKAKSQ 78

RESULT 7  
 AAR30859 standard; Protein: 78 AA.

AC AAR30859;  
 XX  
 XX 09-JUN-1993 (first entry)  
 DT XX  
 DE Leu8 hPTH (7-84) mutein.  
 XX  
 XX Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;  
 KW hypercalcaemia.  
 XX  
 XX Synthetic.

PH Key Location/Qualifiers  
 FT Region 2 /note= "Met -> Leu"  
 FT  
 XX  
 XX EP528271-A.  
 PN  
 PD 24-FEB-1993.

XX 05-AUG-1992; 92EP-0113322.  
 XX  
 XX 07-AUG-1991; 91JP-0198056.  
 PR 26-JUN-1992; 92JP-0169713.  
 XX  
 XX (TAKE ) TAKEPA CHEM IND LTD.  
 PA  
 PI Fukuda T;  
 PI  
 XX  
 DR WPI: 1993-060187/08.  
 DR N-PSDB; AAO36836.

XX New human parathyroid mutein(s) - useful for treating e.g.  
 PT osteoporosis, hypoparathyroidism, hyperparathyroidism,  
 PT hypercalcaemia, hypertension etc.  
 XX

PS Example: Page 22; 88pp; English.

CC The sequence is that of mutated human parathyroid hormone (hPTH)  
 CC (7-84) where Met8 is substid. by Leu. It has higher stability, enhanced  
 CC activity and improved absorption by tissues. It can act as a PTH  
 CC antagonist and can be used as a therapeutic agent for hypercalcaemia  
 CC and hyperparathyroidism.  
 CC  
 XX

SQ Sequence 78 AA;

Query Match 98.0%; Score 248; DB 14; Length 78;  
 Best Local Similarity 98.0%; Pred. No. 6.5e-26;  
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 28 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEADKADVNLTKAKSQ 78

RESULT 8  
 AAE23725 standard; peptide: 78 AA.

XX AAE23725;  
 XX  
 XX 10-SEP-2002 (first entry)  
 DT  
 XX Human parathyroid hormone (hPTH) peptide (7-84).  
 DE

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;  
 KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;  
 KW acne; actinic keratosis; alopecia; gene therapy.  
 XX  
 XX Homo sapiens.

XX WO200228420-A2.  
 PN  
 XX 11-APR-2002.  
 PD  
 XX

XX 05-OCT-2001; 2001WO-US31082.  
 PE  
 XX 06-OCT-2000; 2000US-238134P.  
 PR

PA (HOLI/) HOLICK M F.

PI Holick MF;  
 XX  
 XX WPI: 2002-452304/48.  
 DR N-PSDB; AAD37995.

XX Regulating mammalian skin or hair cell proliferation and  
 PT differentiation by administering nucleic acids encoding peptides  
 PT derived from N-terminal region of human parathyroid hormone (hPTH) or  
 PT hPTH-related protein  
 XX

Claim 35; Fig 15; 56pp; English.

XX The invention relates to a method for regulating proliferation or  
 CC enhancing differentiation of mammalian skin or hair cell. The method  
 CC involves administering nucleic acids encoding peptides derived from  
 CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related  
 CC peptide (PTHrP). The method is used for inhibiting hyperproliferative  
 CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic  
 CC keratosis, skin cancer, for inhibiting hair growth or preventing hair  
 CC regrowth. It is useful for stimulating cell growth, rejuvenating aged  
 CC skin, preventing skin wrinkles, creating skin wrinkles, enhancing wound  
 CC healing, stimulating hair growth, maintaining hair growth, treating or  
 CC preventing female or male pattern baldness, for treating chemotherapy  
 CC induced alopecia and also for stimulating epidermal cell growth or  
 CC hair follicle cell growth. The method is also used in gene therapy.  
 CC The present sequence is hPTH peptide.  
 CC  
 XX

SQ Sequence 78 AA; %.

Query Match 98.0%; Score 248; DB 23; Length 78;  
 Best Local Similarity 98.0%; Pred. No. 6.5e-26;  
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 28 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEADKADVNLTKAKSQ 78

RESULT 9  
 AAU73024 standard; peptide: 78 AA.

XX AAU73024;  
 XX  
 XX 12-MAR-2002 (first entry)  
 DT  
 XX Parathyroid hormone PTH/PTHrP modulating domain #6.  
 DE

XX Human; parathyroid hormone; PTH; parathyroid hormone-related protein;  
 KW PTHrP; bone resorption inhibitor; osteoprotegerin; OPG; OPG-L antibody;  
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; ibuprofen;  
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;  
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;  
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;  
 KW Gaucher's disease; sickle cell anemia; systemic lupus erythematosus;  
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;  
 KW immunoglobulin G; IgG.

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GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: March 13, 2003, 14:46:09 ; Search time 8.75373 Seconds  
(without alignments)  
171.421 Million cell updates/sec

Title: US-09-636-530-3

Perfect score: 253

Sequence: 1 FVALGAPLAPRADAGSQRPK.....KSLGANKADYNTLTKAKSQ 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCtUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	248	98.0	51	3	US-09-044-536A-7
2	248	98.0	84	1	US-07-863-014-2
3	248	98.0	84	1	US-08-332-453-2
4	248	98.0	84	1	US-08-689-190-2
5	248	98.0	84	2	US-08-835-231-9
6	248	98.0	84	2	US-08-803-918-3
7	248	98.0	84	3	US-09-044-536A-36
8	248	98.0	84	4	US-09-108-661-9
9	248	98.0	84	5	PCT-US95-15800-25
10	243	96.0	84	2	US-08-142-551B-1
11	243	96.0	84	2	US-08-411-726-1
12	238	94.1	84	1	US-07-707-114-1
13	237	93.7	50	2	US-08-142-551B-119
14	209	82.6	78	2	US-08-733-446-1
15	209	82.6	79	2	US-08-733-446-2
16	209	82.6	80	3	US-08-733-446-3
17	209	82.6	81	2	US-08-733-446-4
18	209	82.6	84	2	US-08-733-446-5
19	199	78.7	84	1	US-07-773-098-1
20	199	78.7	84	1	US-07-773-098-2
21	199	78.7	84	1	US-07-773-098-7
22	199	78.7	84	1	US-07-773-098-8
23	199	78.7	84	1	US-07-773-098-9
24	199	78.7	84	1	US-07-773-098-10
25	194	76.7	84	1	US-07-776-272-14
26	58	22.9	1120	4	US-09-147-404-1
27	55	21.7	1886	4	US-08-938-105-3

28	54.5	21.5	801	4	US-09-134-001C-5584	Sequence 5584, Ap
29	52.5	20.8	185	4	US-09-154-083-14	Sequence 14, Appl
30	52	20.6	133	4	US-08-961-083-188	Sequence 188, App
31	52	20.6	287	1	US-08-624-125-17	Sequence 17, Appl
32	51	20.2	706	2	US-08-339-152A-29	Sequence 29, Appl
33	51	20.2	706	2	US-08-007-999B-4	Sequence 4, Appl
34	51	20.2	706	2	US-08-689-276A-4	Sequence 4, Appl
35	51	20.2	763	1	US-08-155-331-13	Sequence 13, Appl
36	51	20.2	763	1	US-08-424-022-13	Sequence 13, Appl
37	51	20.2	763	2	US-08-424-017B-13	Sequence 13, Appl
38	51	20.2	763	5	PCT-US93-11696-13	Sequence 13, Appl
39	51	20.2	2308	1	US-08-015-973-1	Sequence 1, Appl
40	51	20.2	2308	2	US-08-448-164-1	Sequence 1, Appl
41	51	20.2	2308	4	US-08-081-929-2	Sequence 2, Appl
42	51	20.2	2314	4	US-09-816-703A-2	Sequence 2, Appl
43	51	20.2	10182	4	US-09-134-001C-3159	Sequence 3159, Ap
44	50.5	20.0	602	4	US-09-374-454-19	Sequence 19, Appl
45	50	19.8	592	4	US-09-377-155-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-09-044-536A-7  
; Sequence 7, Application US/09044536A  
; Patent No. 6025467  
; GENERAL INFORMATION:  
; APPLICANT: FUKUDA, Tsunehiko  
; APPLICANT: NAKAGAWA, Shizue  
; APPLICANT: HAHASHITA, Junko  
; APPLICANT: TAKEKUMI, Shigehisa  
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/044,536A  
; FILING DATE: 19-MAR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/662,871  
; FILING DATE: 12-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CONLIN, David G  
; REGISTRATION NUMBER: 27,026  
; REFERENCE/DOCKET NUMBER: 46509-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 51 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: partial peptide  
; LOCATION: 1..51  
; US-09-044-536A-7  
Query Match 98.0%; Score 248; DB 3; Length 51;  
Best Local Similarity 98.0%; Pred. No. 5e-28;





ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAMS, Gregory D  
REGISTRATION NUMBER: 30,901  
REFERENCE/DOCKET NUMBER: 41,288  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEFAX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-689-190-2

Query Match 98.0%; Score 248; DB 1; Length 84;  
Best Local Similarity 98.0%; Pred. No. 9.5e-28;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEGANKADVNLTKAKSQ 51  
DB 34 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEGANKADVNLTKAKSQ 84

RESULT 5  
US-08-835-231-9  
Sequence 9, Application US/08835231  
Patent No. 5861284  
GENERAL INFORMATION:  
APPLICANT: NISHIMURA, Osamu  
APPLICANT: KURIYAMA, Masato  
APPLICANT: KOYAMA, No. 5861284yuki  
APPLICANT: FUKUDA, Tsunehiko  
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY  
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/835,231  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,709  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: 07/838,857  
FILING DATE: 18-FEB-1992  
APPLICATION NUMBER: JP 024841  
FILING DATE: 19-FEB-1991  
APPLICATION NUMBER: JP 0271438  
FILING DATE: 18-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: DAVID, RESNICK S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 41614-FWC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEFAX: 200291 STRE  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-835-231-9

Query Match 98.0%; Score 248; DB 2; Length 84;  
Best Local Similarity 98.0%; Pred. No. 9.5e-28;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEGANKADVNLTKAKSQ 51  
DB 34 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEGANKADVNLTKAKSQ 84

RESULT 6  
US-08-805-918-3  
Sequence 3, Application US/08805918  
Patent No. 585821  
GENERAL INFORMATION:  
APPLICANT: MAGOTA, Koji  
APPLICANT: MASUDA, Toyofumi  
APPLICANT: SUZUKI, Yui  
APPLICANT: YABUTA, Masayuki  
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF SECRETORY KEX2  
TITLE OF INVENTION: DERIVATIVES  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/805,918  
FILING DATE: 04-MAR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-073217  
FILING DATE: 04-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-352580  
FILING DATE: 16-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 001560-295  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-6620  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-805-918-3

Query Match 98.0%; Score 248; DB 2; Length 84;  
Best Local Similarity 98.0%; Pred. No. 9.5e-28;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEANKADVNLTKAKSQ 51  
Db 34 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEADKADVNLTKAKSQ 84

RESULT 7  
US-09-044-536A-36  
Sequence 36, Application US/09044536A  
Patent No. 6025467  
GENERAL INFORMATION:  
APPLICANT: FUKUDA, Tsunehiko  
APPLICANT: MAKAGAWA, Shizue  
APPLICANT: HABASHITA, Junko  
APPLICANT: TAKEOTOMI, Shigehisa  
TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/044,536A  
FILING DATE: 19-MAR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/662,871  
FILING DATE: 12-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: COHLIN, David G.  
REGISTRATION NUMBER: 27,026  
REFERENCE/DOCKET NUMBER: 46509-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
INFORMATION FOR SEQ. ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: Xaa=acidic amino acid;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: Xaa=hydrophobic alpha amino acid, basic  
OTHER INFORMATION: amino acid;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: Xaa=Gly, Ala, Ser, Lys, Orn;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 13  
OTHER INFORMATION: Xaa= basic amino acid;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 14  
OTHER INFORMATION: Xaa= basic amino acid;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 15  
OTHER INFORMATION: Xaa= aliphatic neutral amino acid, basic

OTHER INFORMATION: amino acid;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 16,17  
OTHER INFORMATION: Xaa= non-charged hydrophilic amino acid-  
OTHER INFORMATION: basic amino acid;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 19  
OTHER INFORMATION: Xaa= acidic amino acid, basic amino acid;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 21  
OTHER INFORMATION: Xaa= aliphatic neutral amino acid, basic  
OTHER INFORMATION: amino acid;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 26  
OTHER INFORMATION: Xaa= basic amino acid;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 27  
OTHER INFORMATION: Xaa= non-charged hydrophilic amino acid,  
OTHER INFORMATION: basic amino acid;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 30  
OTHER INFORMATION: Xaa= acidic amino acid, aliphatic neutral  
OTHER INFORMATION: amino acid;  
US-09-044-536A-36

Query Match 98.0%; Score 248; DB 3; Length 84;  
Best Local Similarity 98.0%; Pred. No. 9, 5e-28;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEANKADVNLTKAKSQ 51  
Db 34 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEADKADVNLTKAKSQ 84

RESULT 8  
US-09-108-661-9  
Sequence 9, Application US/09108661  
Patent No. 6287806  
GENERAL INFORMATION:  
APPLICANT: NISHIMURA, Osamu  
APPLICANT: KURIYAMA, Masato  
APPLICANT: FUKUDA, Tsunehiko  
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY  
ACTIVE RECOMBINANT CYSTEINE-FREE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/108,661  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,709  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: 07/838,857  
FILING DATE: 18-FEB-1992

APPLICATION NUMBER: JP 024841  
FILING DATE: 19-FEB-1991  
APPLICATION NUMBER: JP 0271438  
FILING DATE: 18-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: DAVID, RESNICK S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 41614-FWC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: 20291 STRE  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-09-108-661-9

Query Match 98.0%; Score 248; DB 4; Length 84;  
Best Local Similarity 98.0%; Pred. No. 9.5e-28;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 34 FVALGAPLAPRDAGSORPRKKEDNVLVESHESKSLGANKADYVLTAKSQ 84

Query 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHESKSLGANKADYVLTAKSQ 51  
|||||  
Db 34 FVALGAPLAPRDAGSORPRKKEDNVLVESHESKSLGANKADYVLTAKSQ 84

RESULT 9  
PCT-US95-15800-25  
Sequence 25, Application PC/TUS9515800  
GENERAL INFORMATION:  
APPLICANT: Bionbraska, Inc.  
TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING  
NUMBER OF INVENTION: RECOMBINANT FUSION PROTEIN CONSTRUCTS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 Norwest Center, 90 S. 7th Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: U.S.A.  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/15800  
FILING DATE: 07-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,530  
FILING DATE: 07-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.45USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/332-5300  
TELEFAX: 612/332-9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
PCT-US95-15800-25

Query Match 98.0%; Score 248; DB 5; Length 84;  
Best Local Similarity 98.0%; Pred. No. 9.5e-28;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 34 FVALGAPLAPRDAGSORPRKKEDNVLVESHESKSLGANKADYVLTAKSQ 84

Query 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHESKSLGANKADYVLTAKSQ 51  
|||||  
Db 34 FVALGAPLAPRDAGSORPRKKEDNVLVESHESKSLGANKADYVLTAKSQ 84

RESULT 10  
US-08-142-551B-1  
Sequence 1, Application US/08142551B  
Patent No. 5814603  
GENERAL INFORMATION:  
APPLICANT: Oldenburg, Kevin R.  
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: US  
ZIP: 22313  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,551B  
FILING DATE: 25-OCT-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/077,296  
FILING DATE: 14-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,219  
FILING DATE: 12-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,677  
FILING DATE: 22-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 000324-010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 854-7400  
TELEFAX: (415) 854-8275  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..84  
OTHER INFORMATION: /note="84 amino acid PTH"  
US-08-142-551B-1

Query Match 96.0%; Score 243; DB 2; Length 84;

Best Local Similarity 96.1%; Pred. No. 4.8e-27;  
Matches 49; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLARDAGSORPRKEDNVLSHESKSLGEGANKADVNLTKAKSQ 51  
DB 34 FVALGAPLARDAGSORPRKEDNVLSHESKSLGEGANKADVNLTKAKSQ 84

RESULT 11

US-08-411-726-1  
Sequence 1, Application US/08411726  
Patent No. 5880093

GENERAL INFORMATION:

APPLICANT: BACNOLI, Franco

TITLE OF INVENTION: Use of Parathormone, Its Biologically

TITLE OF INVENTION: Active Fragments and Correlated Peptides, for the Preparation

TITLE OF INVENTION: Pharmaceutical Compositions useful for the Treatment of Pregn

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenyon & Kenyon

STREET: 1 Broadway

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10004

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 6.2

SOFTWARE: Wordperfect 6.1 for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/411,726

FILING DATE: 05-APR-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/02755

FILING DATE: 08-OCT-1993

APPLICATION NUMBER: MI-92A002331

FILING DATE: 09-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: PALMESE, Maria Luisa

REGISTRATION NUMBER: 34,402

REFERENCE/DOCKET NUMBER: 2111/1300

TELEPHONE: 212-425-7200

TELEFAX: 212-425-5288

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-411-726-1

Query Match

Best Local Similarity 96.1%; Pred. No. 4.8e-27;

Matches 49; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLARDAGSORPRKEDNVLSHESKSLGEGANKADVNLTKAKSQ 51  
DB 34 FVALGAPLARDAGSORPRKEDNVLSHESKSLGEGANKADVNLTKAKSQ 84

RESULT 12

US-07-707-114-1

Sequence 1, Application US/07707114

Patent No. 5208041

GENERAL INFORMATION:

APPLICANT: SINDREY, Dennis R.

TITLE OF INVENTION: ESSENTIALLY PURE HUMAN PARATHYROID

TITLE OF INVENTION: HORMONE

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/707,114

FILING DATE: 19910523

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16777/147 ALLE

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: homo sapiens

IMMEDIATE SOURCE:

CLONE: hPTH

US-07-707-114-1

Query Match

Best Local Similarity 94.1%; Pred. No. 2.4e-26;

Matches 48; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLARDAGSORPRKEDNVLSHESKSLGEGANKADVNLTKAKSQ 51  
DB 34 FVALGAPLARDAGSORPRKEDNVLSHESKSLGEGANKADVNLTKAKSQ 84

RESULT 13

US-08-142-551B-119

Sequence 119, Application US/08142551B

Patent No. 5814603

GENERAL INFORMATION:

APPLICANT: Oldenburg, Kevin R.

TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND

TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME

NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: 699 Prince Street

CITY: Alexandria

STATE: Virginia

COUNTRY: US

ZIP: 22313

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/142,551B

FILING DATE: 25-OCT-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/077,296

FILED DATE: 14-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,219  
FILING DATE: 12-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,677  
FILING DATE: 22-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 000324-010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 854-7400  
TELEFAX: (415) 854-8275  
INFORMATION FOR SEQ ID NO: 119:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..50  
OTHER INFORMATION: /note="Amino acid residues 34-84  
of Human PTH."  
US-08-142-551B-119

Query Match 93.7%; Score 237; DB 2; Length 50;  
Best Local Similarity 96.0%; Pred. No. 1.7e-26;  
Matches 48; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VALGAPLAPRDAGSQRPKRKEDNVLVESHKSLGSEANKADVNVLTAKSQ 51  
Db 1 VALGAPLAPRDAGSQRPKRKEDNVLVESHKSLGSEANKADVNVLTAKSQ 50

RESULT 14  
US-08-733-446-1  
Sequence 1, Application US/08733446  
Patent No. 5856138  
GENERAL INFORMATION:  
APPLICANT: FUKUDA, Tsunehiko  
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTAINS AND  
TITLE OF INVENTION: PRODUCTION THEREOF  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/733,446  
FILING DATE: 18-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/402,970  
FILING DATE: US/07/926,787  
APPLICATION NUMBER: US/07/926,787  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: NEUNER, George W  
REGISTRATION NUMBER: 26964  
REFERENCE/DOCKET NUMBER: 42025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400

TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: mutation  
LOCATION: 2 Xaa-Leu, Ile, Val, Phe, Tyr, Trp or Met,  
LOCATION: 12 Xaa-Leu, Ile, Val, Phe, Tyr, Trp or Met,  
LOCATION: 28 Xaa-Cys or Phe, 29 Xaa-Cys or Val,  
LOCATION: 31 Xaa-Cys or Leu, 33 Xaa-Cys or Ala,  
LOCATION: 35 Xaa-Cys or Leu, 37 Xaa-Cys or Pro, 38 Xaa-Cys or Arg  
IDENTIFICATION METHOD: E  
US-08-733-446-1

Query Match 82.6%; Score 209; DB 2; Length 78;  
Best Local Similarity 87.8%; Pred. No. 2.7e-22;  
Matches 43; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ALGAPLAPRDAGSQRPKRKEDNVLVESHKSLGSEANKADVNVLTAKSQ 51  
Db 30 AXGXPPAXXXDAGSQRPKRKEDNVLVESHKSLGSEANKADVNVLTAKSQ 78

RESULT 15  
US-08-733-446-2  
Sequence 2, Application US/08733446  
Patent No. 5856138  
GENERAL INFORMATION:  
APPLICANT: FUKUDA, Tsunehiko  
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTAINS AND  
TITLE OF INVENTION: PRODUCTION THEREOF  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/733,446  
FILING DATE: 18-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/402,970  
FILING DATE: US/07/926,787  
APPLICATION NUMBER: US/07/926,787  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: NEUNER, George W  
REGISTRATION NUMBER: 26964  
REFERENCE/DOCKET NUMBER: 42025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 79 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:



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OM protein - protein search, using sw model

Run on: March 13, 2003, 14:52:29 ; Search time 24.3582 Seconds

(Without alignments)  
278.993 Million cell updates/sec

Title: US-09-636-530-3

Perfect score: 253

Sequence: 1 FVALGAPLAPRDAGSQRP...KSLGKANKADVNLTKAKSQ 51

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
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17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	253	100.0	51	21	AA07466
2	253	100.0	82	21	AA07465
3	253	100.0	84	21	AA07464
4	248	98.0	51	18	AA08107
5	248	98.0	55	12	AA08107
6	248	98.0	78	14	AA08107
7	248	98.0	78	14	AA08107
8	248	98.0	78	23	AA08107
9	248	98.0	78	23	AA08107
10	248	98.0	79	14	AA08107

11	248	98.0	80	14	AA03232	hPTH mutein lackin
12	248	98.0	81	14	AA030854	hPTH mutein lackin
13	248	98.0	84	13	AA03790	parathyroid hormon
14	248	98.0	84	13	AA03571	human PTH encoded
15	248	98.0	84	13	AA02845	oxidation resistan
16	248	98.0	84	13	AA02846	oxidation resistan
17	248	98.0	84	13	AA02847	oxidation resistan
18	248	98.0	84	13	AA02848	oxidation resistan
19	248	98.0	84	13	AA02951	oxidation resistan
20	248	98.0	84	13	AA02952	oxidation resistan
21	248	98.0	84	13	AA02953	oxidation resistan
22	248	98.0	84	13	AA02954	oxidation resistan
23	248	98.0	84	13	AA02955	oxidation resistan
24	248	98.0	84	13	AA02956	oxidation resistan
25	248	98.0	84	13	AA02957	oxidation resistan
26	248	98.0	84	13	AA02958	oxidation resistan
27	248	98.0	84	14	AA030850	Leu18 hPTH mute
28	248	98.0	84	14	AA030857	human parathyroid
29	248	98.0	84	14	AA042067	stability-enhanced
30	248	98.0	84	14	AA042068	stability-enhanced
31	248	98.0	84	14	AA042069	stability-enhanced
32	248	98.0	84	14	AA042070	stability-enhanced
33	248	98.0	84	14	AA042071	stability-enhanced
34	248	98.0	84	14	AA042072	stability-enhanced
35	248	98.0	84	14	AA042073	stability-enhanced
36	248	98.0	84	14	AA042074	stability-enhanced
37	248	98.0	84	14	AA042075	stability-enhanced
38	248	98.0	84	14	AA042076	stability-enhanced
39	248	98.0	84	14	AA042077	stability-enhanced
40	248	98.0	84	15	AA04692	sequence of varian
41	248	98.0	84	15	AA04693	sequence of varian
42	248	98.0	84	15	AA04694	sequence of varian
43	248	98.0	84	15	AA04695	sequence of varian
44	248	98.0	84	15	AA04696	sequence of varian
45	248	98.0	84	17	AA029420	human parathyroid

#### ALIGNMENTS

RESULT 1	AA07466	standard; protein; 51 AA.
ID	AA07466	
XX	AA07466	
AC	AA07466	
DT	20-0CT-2000 (first entry)	
XX		
DE	Amino acid sequence of human parathyroid hormone antagonist.	
XX		
KW	Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200042437-A1.	
XX		
PD	20-JUL-2000.	
XX		
PF	13-JAN-2000; 2000WO-US00855.	
XX		
PR	14-JAN-1999; 99US-0231422.	
XX		
PR	26-JUN-1999; 99US-0344639.	
XX		
FA	(SCAN-) SCANTIBODIES LAB INC.	
XX		
XX	WPI: 2000-476147/41.	
XX		
PT	Differentiating between normal parathyroid function and hyperparathyroidism comprises determining and comparing whole parathyroid hormone, parathyroid hormone inhibitory peptide fragment and/or total parathyroid hormone levels -	
XX		
PS	Disclosure; Page 43; 46pp; English.	

XX The present sequence represents a fragment of human parathyroid  
 CC hormone (PTH), comprising residues 34-84, which functions as a PTH  
 CC antagonist. The specification describes a method for differentiating  
 CC between a person having substantially normal parathyroid function  
 CC and having hyperparathyroidism. The method comprises determining and  
 CC comparing at least two of the following parameters: whole parathyroid  
 CC hormone level, parathyroid hormone inhibitory peptide fragment level  
 CC and total parathyroid hormone level. The method is used for monitoring  
 CC (treatments of) parathyroid related bone disease and the effects of  
 CC therapeutic treatment for hyperparathyroidism.

XX  
 SQ Sequence 51 AA;

Query Match 100.0%; Score 253; DB 21; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-27;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51

RESULT 2

AAAB07465  
 ID AAB07465 standard; protein; 82 AA.

XX  
 AC AAB07465;

XX  
 DT 20-OCT-2000 (first entry)

XX Amino acid sequence of human parathyroid hormone antagonist.

XX Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.

XX Homo sapiens.

XX WO200042437-A1.

XX 20-JUL-2000.

XX 13-JAN-2000; 2000WO-US00855.

XX 14-JAN-1999; 99US-0231422.

XX 26-JUN-1999; 99US-0344639.

XX (SCAN-) SCANTIBODIES LAB INC.

XX WPI; 2000-476147/41.

XX Differentiating between normal parathyroid function and

XX hyperparathyroidism comprises determining and comparing whole

XX parathyroid hormone, parathyroid hormone inhibitory peptide fragment

XX and/or total parathyroid hormone levels -

XX Disclosure; Page 42-43; 46pp; English.

XX The present sequence represents a fragment of human parathyroid

XX hormone (PTH), comprising residues 3-84, which functions as a PTH

XX antagonist. The specification describes a method for differentiating

XX between a person having substantially normal parathyroid function

XX and having hyperparathyroidism. The method comprises determining and

XX comparing at least two of the following parameters: whole parathyroid

XX hormone level, parathyroid hormone inhibitory peptide fragment level

XX and total parathyroid hormone level. The method is used for monitoring

XX (treatments of) parathyroid related bone disease and the effects of

XX therapeutic treatment for hyperparathyroidism.

XX Sequence 82 AA;

Query Match 100.0%; Score 253; DB 21; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-26;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 32 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 82

RESULT 3

AAAB07464  
 ID AAB07464 standard; protein; 84 AA.

XX  
 AC AAB07464;

XX 20-OCT-2000 (first entry)

XX Amino acid sequence of human parathyroid hormone.

XX Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.

XX Homo sapiens.

XX WO200042437-A1.

XX 20-JUL-2000.

XX 13-JAN-2000; 2000WO-US00855.

XX 14-JAN-1999; 99US-0231422.

XX 26-JUN-1999; 99US-0344639.

XX (SCAN-) SCANTIBODIES LAB INC.

XX WPI; 2000-476147/41.

XX Differentiating between normal parathyroid function and

XX hyperparathyroidism comprises determining and comparing whole

XX parathyroid hormone, parathyroid hormone inhibitory peptide fragment

XX and/or total parathyroid hormone levels -

XX Disclosure; Fig 1; 46pp; English.

XX The present sequence represents a human parathyroid hormone (PTH).

XX Fragments of PTH function as PTH antagonists. The specification

XX describes a method for differentiating between a person having

XX substantially normal parathyroid function and having hyperparathyroidism.

XX The method comprises determining and comparing at least two of the

XX following parameters: whole parathyroid hormone level, parathyroid

XX hormone inhibitory peptide fragment level and total parathyroid hormone

XX level. The method is used for monitoring (treatments of) parathyroid

XX related bone disease and the effects of therapeutic treatment for

XX hyperparathyroidism.

XX Sequence 84 AA;

Query Match 100.0%; Score 253; DB 21; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-26;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 34 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

RESULT 4

AAAB08107  
 ID AAB08107 standard; peptide; 51 AA.

XX  
 AC AAB08107;

XX 10-OCT-1997 (first entry)

XX Human parathyroid hormone residues 34-84.

XX Human; parathyroid hormone; PTH; CAMP-producing activity;



KW bone formation; osteoporosis; hypoparathyroidism; hypertension;  
 KW climacteric disturbance.  
 XX  
 OS Synthetic.  
 XX  
 PN EP748817-A2.  
 XX  
 PD 18-DEC-1996.  
 XX  
 PE 13-JUN-1996; 96EP-0109475.  
 XX  
 PR 15-JUN-1995; 95JP-0148652.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;  
 DR WPI; 1997-036114/04.  
 XX  
 PT New parathyroid hormone derivs. - useful in treatment of bone  
 PT diseases, hypoparathyroidism and hypertension  
 PS  
 PS Claim 3; Page 39; 42pp; English.  
 XX  
 CC The sequences given in AAM08103-07 represent fragments of human para-  
 CC thyroid hormone (PTH) which were used as Xaa34 in the generic sequence  
 CC given in AAM08102. Peptides based on the generic sequence are human PTH  
 CC (1-34) derivative peptides. They have potent cAMP-producing activity and  
 CC bone formation activity. They may be used in treatment of bone  
 CC diseases including osteoporosis, hypoparathyroidism, hypertension  
 CC and climacteric disturbance. The peptides are low in toxicity and  
 CC are safe.  
 CC  
 XX  
 SO Sequence 51 AA:

Query Match 98.0%; Score 248; DB 18; Length 51;  
 Best Local Similarity 98.0%; Pred. No. 3.8e-26;  
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLSHEKSLGEANKADYNTLTKAKSQ 51  
 DB 1 FVALGAPLAPRDAGSORPRKKEDNVLSHEKSLGEADKADYNTLTKAKSQ 51

## RESULT 5

AAR11732  
 ID AAR11732 standard; Protein: 55 AA.

AC AAR11732;

DT 03-JUL-1991 (first entry)

DE PTH-(29-84).

KW Parathyroid hormone; calcium; osteoporosis; bone.

OS Synthetic.

PN W09105050-A.

PD 18-APR-1991.

PE 01-OCT-1990; 90WO-C000335.

PR 29-SEP-1989; 89CA-2615001.

PA (CANA ) NAT RES COUNCIL CAN.

PI Sung WL;

DR WPI; 1991-132857/18.

DR N-PSDB; AAQ11618.

PT Mature human parathyroid synthesis - includes using eg E. coli  
 PT transformed by plasmid contg. synthetic nucleotide sequence contg.  
 PT adenine rich codons in N-terminal region.  
 XX  
 PS Disclosure; Fig 6; 62pp; English.  
 XX  
 CC Codons 29-84 are degenerate in the usage frequency favoured by  
 CC E. coli or yeast. Codons 1-28 (see AAQ11617) are designed to contain  
 CC adenine rich codons. The sequence is prepd. from eight oligo-  
 CC nucleotides (4 on each strand). A plasmid contg. the complete  
 CC sequence expresses PTH with an improved yield. PTH is a blood  
 CC calcium regulator known to increase bone mass.  
 CC  
 XX  
 SO Sequence 55 AA:

Query Match 98.0%; Score 248; DB 12; Length 55;  
 Best Local Similarity 98.0%; Pred. No. 4.2e-26;  
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLSHEKSLGEANKADYNTLTKAKSQ 51  
 DB 5 FVALGAPLAPRDAGSORPRKKEDNVLSHEKSLGEADKADYNTLTKAKSQ 55

RESULT 6  
 AAR30852  
 ID AAR30852 standard; Protein: 78 AA.

AC AAR30852;

DT 09-JUN-1993 (first entry)

DE hPTH mutlein lacking 6 N-terminal amino acids.

KW Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;  
 KW hypercalcaemia.

OS Synthetic.

PN EP528271-A.

PD 24-FEB-1993.

PE 05-AUG-1992; 92EP-0113322.

PR 07-AUG-1991; 91JP-0198056.

PR 26-JUN-1992; 92JP-0169713.

PA (TAKE ) TAKEDA CHEM IND LTD.

PI Fukuda T;

DR WPI; 1993-060187/08.

DR N-PSDB; AAQ35228.

PT New human parathyroid mutlein(s) - useful for treating e.g.  
 PT osteoporosis, hypoparathyroidism, hyperparathyroidism,  
 PT hypercalcaemia, hypertension etc.

PS Disclosure; Page 7; 88pp; English.

CC The sequence is that of a human parathyroid hormone (hPTH) peptide  
 CC lacking 6 hPTH N-terminal amino acids. The peptide can have higher  
 CC stability, enhanced activity and improved absorption by tissues.  
 CC It can act as a PTH antagonist and can be used as a therapeutic  
 CC agent for hypercalcaemia and hyperparathyroidism.  
 CC  
 XX  
 SO Sequence 78 AA:

Query Match 98.0%; Score 248; DB 14; Length 78;  
 Best Local Similarity 98.0%; Pred. No. 6.5e-26;  
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKASQ 51  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 28 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEADKADVNLTKASQ 78  
 XX

## RESULT 7

AAE30859  
 ID AAR30859 standard; Protein; 78 AA.

XX AAR30859;

DT 09-JUN-1993 (first entry)

DE Leu8 hPTH (7-84) mutein.

KW Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;  
 hypercalcaemia.

XX Synthetic.

FT Key Location/Qualifiers  
 FT Region 2  
 FT /note= "Met -> Leu"

PN EP528271-A.

PD 24-FEB-1993.

PF 05-AUG-1992; 92EP-0113322.

PR 07-AUG-1991; 91JP-0198056.

PR 26-JUN-1992; 92JP-0169713.

PA (TAKE ) TAKEDA CHEM IND LTD.

PI Fukuda T;

DR WPI: 1993-060187/08.

DR N-PSDB: AAO36836.

PT New human parathyroid mutein(s) - useful for treating e.g.  
 PT osteoporosis, hypoparathyroidism, hyperparathyroidism,  
 PT hypercalcaemia, hypertension etc.

PS Example: Page 22; 88pp; English.

CC The sequence is that of mutated human parathyroid hormone (hPTH)  
 CC (7-84) where Met8 is substd. by Leu. It has higher stability, enhanced  
 CC activity and improved absorption by tissues. It can act as a PTH  
 CC antagonist and can be used as a therapeutic agent for hypercalcaemia  
 CC and hyperparathyroidism.

CC and hyperparathyroidism.

XX Sequence 78 AA:

SO

Query Match 98.0%; Score 248; DB 14; Length 78;  
 Best Local Similarity 98.0%; Pred. No. 6.5e-26;

Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKASQ 51  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 28 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEADKADVNLTKASQ 78

XX

## RESULT 8

AAE23725  
 ID AAE23725 standard; Peptide; 78 AA.

XX AAE23725;

DT 10-SEP-2002 (first entry)

DE Human parathyroid hormone (hPTH) peptide (7-84).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;  
 KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;  
 KW acne; actinic keratosis; alopecia; gene therapy.

OS Homo sapiens.

PN WO200228420-A2.

PD 11-APR-2002.

PF 05-OCT-2001; 2001WO-US31082.

PR 06-OCT-2000; 2000US-238134P.

PA (HOLI/) HOLICK M F.

PI Holick MF;

DR WPI: 2002-452304/48.

DR N-PSDB: AAD37995.

PT Regulating mammalian skin or hair cell proliferation and  
 PT differentiation by administering nucleic acids encoding peptides  
 PT derived from N-terminal region of human parathyroid hormone (hPTH) or  
 PT hPTH-related protein

PS Claim 35; Fig 15; 56pp; English.

XX

CC The invention relates to a method for regulating proliferation or  
 CC enhancing differentiation of mammalian skin or hair cell. The method

CC involves administering nucleic acids encoding peptides derived from  
 CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related

CC peptide (PTHrP). The method is used for inhibiting hyperproliferative  
 CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic

CC keratosis, skin cancer, for inhibiting hair growth or preventing hair  
 CC regrowth. It is useful for stimulating cell growth, rejuvenating aged

CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound  
 CC healing, stimulating hair growth, maintaining hair growth, treating or

CC preventing female or male pattern baldness, for treating chemotherapy  
 CC induced alopecia and also for stimulating epidermal cell growth or

CC hair follicle cell growth. The method is also used in gene therapy.

XX The present sequence is hPTH peptide.

SO Sequence 78 AA:

Query Match 98.0%; Score 248; DB 23; Length 78;  
 Best Local Similarity 98.0%; Pred. No. 6.5e-26;

Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKASQ 51  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 28 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEADKADVNLTKASQ 78

XX

AAU73024  
 ID AAU73024 standard; Peptide; 78 AA.

XX AAU73024;

DT 12-MAR-2002 (first entry)

DE Parathyroid hormone PTH/PTHrP modulating domain #6.

KW Human: parathyroid hormone; PTH; parathyroid hormone-related protein;  
 KW PTHrP; bone resorption inhibitor; osteoprotegerin; OPG; OPG-L antibody;  
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; fibronectin;  
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;  
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;  
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;  
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;  
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;  
 KW immunoglobulin G; IgG.

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XX OS Homo sapiens.
XX PN MO200181415-A2.
XX PD 01-NOV-2001.
XX PF 27-APR-2001; 2001WO-US13528.
XX PR 27-APR-2000; 2000US-200053P.
XX PR 28-JUN-2000; 2000US-214860P.
XX PR 06-FEB-2001; 2001US-266673P.
XX PR 26-APR-2001; 2001US-0843221.
XX PA (AMGE-) AMGEN INC.
XX PI Kostenuik P, Liu C, Lacey DL.
XX DR WPI, 2002-066435/09.
XX PT Composition, useful for treating osteopenia, comprises parathyroid
XX PT hormone and parathyroid hormone-related protein receptor modulators -
XX PS Disclosure; Page 26; 107pp; English.
XX XX
XX CC The invention relates to a composition (I) comprising modulators of
XX CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
XX CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
XX CC comprising PTH agonist optionally with a bone resorption inhibitor, such
XX CC as osteoprotegerin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
XX CC oestrogens, oestrogen receptor modulators and tibolone is useful for
XX CC treating osteopenia. (I) is useful for therapeutic and prophylactic
XX CC purposes. Antagonists of PTH receptor are useful in treating primary and
XX CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
XX CC particularly breast and prostate cancer, cachexia and anorexia,
XX CC osteopenia, including various forms of osteoporosis, Paget's disease of
XX CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
XX CC traumatic injury or nontraumatic necrosis associated with Gaucher's
XX CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
XX CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
XX CC useful as therapeutic agents in conditions including fracture repair
XX CC (including healing of non-union fractures), osteopenia, including various
XX CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
XX CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
XX CC related amino acid sequences of the invention.
XX SQ Sequence 78 AA:
XX
XX Query Match 98.0%; Score 248; DB 23; Length 78;
XX Best Local Similarity 98.0%; Pred. No. 6.5e-26;
XX Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEANKADNVNLTAKSQ 51
DB 28 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEADKADNVNLTAKSQ 78

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XX PD 24-FEB-1993.
XX PF 05-AUG-1992; 92EP-0113322.
XX PR 07-AUG-1991; 91JP-0198056.
XX PR 26-JUN-1992; 92JP-0169713.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Fukuda T;
XX DR WPI, 1993-060187/08.
XX DR N-PSDB; AAQ35229.
XX PT New human parathyroid mutin(s) - useful for treating e.g.
XX PT osteoporosis, hypoparathyroidism, hyperparathyroidism,
XX PT hypercalcaemia, hypertension etc.
XX PS Disclosure; Page 7; 88pp; English.
XX XX
XX CC The sequence is that of a human parathyroid hormone (hPTH) peptide
XX CC lacking 5 hPTH N-terminal amino acids. The peptide can have higher
XX CC stability, enhanced activity and improved absorption by tissues.
XX CC It can act as a PTH antagonist and can be used as a therapeutic
XX CC agent for hypercalcaemia and hyperparathyroidism.
XX SQ Sequence 79 AA:
XX
XX Query Match 98.0%; Score 248; DB 14; Length 79;
XX Best Local Similarity 98.0%; Pred. No. 6.6e-26;
XX Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEANKADNVNLTAKSQ 51
DB 29 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGEADKADNVNLTAKSQ 79

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XX RESULT 11
XX ID AAR35232 standard; Protein; 80 AA.
XX AC AAR35232;
XX XX
XX DT 09-JUN-1993 (first entry)
XX DE hPTH mutin lacking 4 N-terminal amino acids.
XX KW Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;
XX KW hypercalcaemia.
XX OS Synthetic.
XX PN EP528271-A.
XX PD 24-FEB-1993.
XX PF 05-AUG-1992; 92EP-0113322.
XX PR 07-AUG-1991; 91JP-0198056.
XX PR 26-JUN-1992; 92JP-0169713.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Fukuda T;
XX DR WPI, 1993-060187/08.
XX DR N-PSDB; AAQ35230.
XX PT New human parathyroid mutin(s) - useful for treating e.g.
XX PT osteoporosis, hypoparathyroidism, hyperparathyroidism,
XX PT hypercalcaemia, hypertension etc.
XX PN EP528271-A.

```

PS Disclosure; Page 7; 88pp; English.

CC The sequence is that of a human parathyroid hormone (hPTH) peptide  
CC lacking 4 hPTH N-terminal amino acids. The peptide can have higher  
CC stability, enhanced activity and improved absorption by tissues.  
CC It can act as a PTH antagonist and can be used as a therapeutic  
CC agent for hypercalcaemia and hyperparathyroidism.

XX  
SQ Sequence 80 AA;

Query Match 98.0%; Score 248; DB 14; Length 80;  
Best Local Similarity 98.0%; Pred. No. 6.7e-26;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGGEANKADVNLTKAKSQ 51  
DB 30 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGGEANKADVNLTKAKSQ 80

RESULT 12  
AAR30854

ID AAR30854 standard; Protein; 81 AA.

XX  
AC AAR30854;

DT 09-JUN-1993 (first entry)

XX hPTH mutein lacking 3 N-terminal amino acids.

DE Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;  
XX hypercalcaemia.

XX  
OS Synthetic.

XX  
PN EP528271-A.

XX  
PD 24-FEB-1993.

XX  
PF 05-AUG-1992; 92EP-0113322.

XX  
PR 07-AUG-1991; 91JP-0198056.

XX  
PR 26-JUN-1992; 92JP-0169713.

XX  
PA (TAKE ) TAKEDA CHEM IND LTD.

XX  
PI Fukuda T;

XX  
DR WPI: 1993-060187/08.

DR  
N-PSDB: AAQ36829.

XX  
PT New human parathyroid mutein(s) - useful for treating e.g.  
PT osteoporosis, hypoparathyroidism, hyperparathyroidism,  
PT hypercalcaemia, hypertension etc.

XX  
PS Disclosure; Page 7; 88pp; English.

CC The sequence is that of a human parathyroid hormone (hPTH) peptide  
CC lacking 3 hPTH N-terminal amino acids. The peptide can have higher  
CC stability, enhanced activity and improved absorption by tissues.  
CC It can act as a PTH antagonist and can be used as a therapeutic  
CC agent for hypercalcaemia and hyperparathyroidism.

XX  
SQ Sequence 81 AA;

Query Match 98.0%; Score 248; DB 14; Length 81;  
Best Local Similarity 98.0%; Pred. No. 6.8e-26;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGGEANKADVNLTKAKSQ 51  
DB 31 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGGEANKADVNLTKAKSQ 81

.. RESULT 13

AAR23790

ID AAR23790 standard; Protein; 84 AA.

XX  
AC AAR23790;

DT 03-NOV-1992 (first entry)

XX Parathyroid hormone gene product.

DE hPTH; hypoparathyroidism; osteoporosis.

XX  
OS Synthetic.

XX  
PN EP483509-A.

XX  
PD 06-MAY-1992.

XX  
PF 25-SEP-1991; 91EP-0116281.

XX  
PR 28-SEP-1990; 90JP-0257491.

XX  
PR 20-MAR-1991; 91JP-0056434.

XX  
PA (TAKE ) TAKEDA CHEM IND LTD.

XX  
PI Fukuda T, Oshika Y, Yamada T;

XX  
DR WPI: 1992-152248/19.

DR  
N-PSDB: AAQ24478.

XX  
PT Synthetic gene encoding human parathyroid hormone - formed by  
PT ligating oligo-nucleotide(s) and expressed at high yield in E

XX  
PI coli

XX  
PS Disclosure; Page 21; 33pp; English.

CC The human parathyroid hormone (hPTH) sequence given is the product of  
CC a synthetic gene which corresponds to the amino acid sequence of hPTH.  
CC The DNA sequence was produced by enzymatically ligating  
CC oligodeoxynucleotides. hPTH is an important regulator of calcium  
CC metabolism and has clinical applications. To diseases such as  
CC hypoparathyroidism and osteoporosis. This hPTH can be used as a  
CC therapeutic agent or to study the biological role of hPTH in vivo.

XX  
SQ Sequence 84 AA;

Query Match 98.0%; Score 248; DB 13; Length 84;  
Best Local Similarity 98.0%; Pred. No. 7.1e-26;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGGEANKADVNLTKAKSQ 51  
DB 34 FVALGAPLAPRDAGSORPRKKEDNVLVESHKSLGGEANKADVNLTKAKSQ 84

RESULT 14

AAR25571

ID AAR25571 standard; Protein; 84 AA.

XX  
AC AAR25571;

DT 13-JAN-1993 (first entry)

XX  
DE Human PTH encoded by px.

XX  
KW Parathyroid; hormone; osteoporosis; psoriasis; oxidation;  
XX resistance.

XX  
OS Homo sapiens.

XX  
FH key Location/Qualifiers

FT Misc-difference 8 /note= "see CC"

```

FT Misc-difference 18 /note= "see CC"
XX
XX
XX MO9211286-A.
XX
XX PD 09-JUL-1992.
XX
XX PF 18-DEC-1991; 91WO-CA00451.
XX
XX PR 21-DEC-1990; 90US-0630969.
XX PR 13-DEC-1991; 91US-0806271.
XX
XX (ALLE-) ALLELIX BIOPHARMACEUTICALS INC.
XX (GLAX ) GLAXO CANADA INC.
XX
XX PI Bozatto RP, Kronis KA;
XX
XX WPI; 1992-250028/30.
XX DR N-PSDB; AAQ26498.
XX
XX PT New oxidn. resistant variants of parathyroid hormone - used for
XX treating osteoporosis, psoriasis and cardiovascular disorders
XX
XX PS Disclosure; Fig 1; 40pp; English.
XX
XX CC Variants of PTH exhibiting PTH activity and reduced sensitivity
XX to oxidation are obtained by replacing at least one Met residue in
XX PTH (positions 8 and 18) with a genetically encoded amino acid,
XX other than Met and Cys.
XX CC The Met amino acids are indicated in the Features Table.
XX CC The variant may be obtd. using recombinant technique, and may be
XX used for treating osteoporosis, other bone-related disorders,
XX psoriasis and cardiovascular disorders.
XX CC Human PTH refers to the mature form of the hormone, which consists
XX of 84 amino acids arranged in the sequence reported by Kimura et al,
XX CC 1983, Biochem. Biophys. Res. Comm., 114(2):493.
XX CC Examples of variants are given in AAR28845-48 and AAR29561-69.
XX
XX SQ Sequence 84 AA:
XX
XX Query Match 98.0%; Score 248; DB 13; Length 84;
XX Best Local Similarity 98.0%; Pred. No. 7.1e-26;
XX Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHKSLGSEANKADVNVLTAKSQ 51
DB 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHKSLGSEADKADVNVLTAKSQ 84

```

## RESULT 15

AAR28845  
ID AAR28845 standard; Protein; 84 AA.

AC AAR28845;

DT 13-JAN-1993 (first entry)

DE Oxidation resistant PTH variant (1).

XX Parathyroid; hormone; osteoporosis; psoriasis; oxidation;

KW resistance.

XX Homo sapiens.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 8

FT /label= ALA, VAL, LEU, ILE, SER, TRP

XX /note= "pref. Val, Leu or Ile"

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PF 18-DEC-1991; 91WO-CA00451.
XX
XX PR 21-DEC-1990; 90US-0630969.
XX PR 13-DEC-1991; 91US-0806271.
XX
XX (ALLE-) ALLELIX BIOPHARMACEUTICALS INC.
XX (GLAX ) GLAXO CANADA INC.
XX
XX PI Bozatto RP, Kronis KA;
XX
XX WPI; 1992-250028/30.
XX DR
XX
XX PT New oxidn. resistant variants of parathyroid hormone - used for
XX treating osteoporosis, psoriasis and cardiovascular disorders
XX
XX PS Claim 2-4; Page 30; 40pp; English.
XX
XX CC Variants of PTH exhibiting PTH activity and reduced sensitivity
XX to oxidation are obtained by replacing at least one Met residue in
XX PTH (positions 8 and 18) with a genetically encoded amino acid,
XX other than Met and Cys (see AAQ26498).
XX CC The variant may be obtd. using recombinant technique, and may be
XX used for treating osteoporosis, other bone-related disorders,
XX psoriasis and cardiovascular disorders.
XX CC Examples of variants are given in AAR28845-48 and AAR29561-69.
XX
XX SQ Sequence 84 AA:
XX
XX Query Match 98.0%; Score 248; DB 13; Length 84;
XX Best Local Similarity 98.0%; Pred. No. 7.1e-26;
XX Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHKSLGSEANKADVNVLTAKSQ 51
DB 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHKSLGSEADKADVNVLTAKSQ 84

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Search completed: March 13, 2003, 15:00:26  
Job time : 25.3582 secs

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 13, 2003, 14:51:54 ; Search time 13.6269 Seconds  
(without alignments)  
280.743 Million cell updates/sec

Title: US-09-636-530-2  
Perfect score: 422  
Sequence: 1 VSEIQLMHLGKHLNSMERV.....KSLGEANKADVNLTKAKSQ 83

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\*

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2: /cgn2_6/ptodata/1/pubppaa/PCr_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/PCrUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	422	100.0	83	US-09-928-047B-1	Sequence 1, Appli
2	422	100.0	84	US-09-928-047B-5	Sequence 5, Appli
3	418	99.1	82	US-09-928-047B-2	Sequence 2, Appli
4	417	98.8	84	US-09-843-221A-10	Sequence 10, Appli
5	417	98.8	84	US-09-169-786-1	Sequence 1, Appli
6	400	93.6	78	US-09-928-047B-4	Sequence 12, Appli
7	395	93.6	78	US-09-843-221A-12	Sequence 4, Appli
8	359	85.1	84	US-09-879-257A-49	Sequence 49, Appli
9	315	74.6	84	US-09-843-221A-11	Sequence 11, Appli
10	286	67.8	57	US-09-928-047B-8	Sequence 8, Appli
11	253	60.0	51	US-09-928-047B-3	Sequence 3, Appli
12	247	58.5	59	US-09-928-047B-7	Sequence 7, Appli
13	224	53.1	44	US-09-843-221A-13	Sequence 13, Appli
14	193	45.7	37	US-09-843-221A-15	Sequence 15, Appli
15	193	45.7	38	US-09-843-221A-14	Sequence 14, Appli
16	193	45.7	38	US-09-169-786-4	Sequence 4, Appli
17	188	44.5	40	US-10-014-162-111	Sequence 11, App
18	175	41.5	34	US-09-928-047B-6	Sequence 6, Appli
19	175	41.5	34	US-09-843-221A-16	Sequence 16, Appli

20	175	41.5	34	9	US-09-843-221A-20	Sequence 20, Appli
21	175	41.5	34	9	US-09-843-221A-161	Sequence 161, App
22	175	41.5	34	10	US-09-169-786-3	Sequence 3, Appli
23	175	41.5	34	12	US-10-016-403-5	Sequence 5, Appli
24	175	41.5	34	12	US-10-097-079-1	Sequence 1, Appli
25	175	41.5	42	9	US-10-024-918-28	Sequence 28, Appli
26	170	40.3	34	9	US-09-843-221A-19	Sequence 19, Appli
27	170	40.3	34	9	US-09-843-221A-164	Sequence 164, App
28	170	40.3	34	12	US-10-016-403-6	Sequence 6, Appli
29	170	40.3	34	12	US-10-016-403-7	Sequence 7, Appli
30	169	40.0	34	9	US-09-843-221A-17	Sequence 17, Appli
31	169	40.0	34	9	US-09-843-221A-18	Sequence 18, Appli
32	169	40.0	34	9	US-09-843-221A-162	Sequence 162, App
33	169	40.0	34	9	US-09-843-221A-163	Sequence 163, Appli
34	167	39.6	34	9	US-09-843-221A-24	Sequence 24, Appli
35	166	39.3	34	9	US-09-843-221A-21	Sequence 21, Appli
36	166	39.3	34	9	US-09-843-221A-22	Sequence 22, Appli
37	162	38.4	32	9	US-09-843-221A-29	Sequence 29, Appli
38	162	38.4	32	9	US-09-843-221A-30	Sequence 30, Appli
39	157	37.2	34	9	US-09-843-221A-23	Sequence 23, Appli
40	157	37.2	34	9	US-09-843-221A-25	Sequence 25, Appli
41	155	36.7	31	9	US-09-843-221A-27	Sequence 27, Appli
42	155	36.7	31	9	US-09-843-221A-165	Sequence 165, App
43	155	36.7	31	10	US-09-169-786-2	Sequence 2, Appli
44	153	36.3	28	9	US-09-843-221A-32	Sequence 32, Appli
45	153	36.3	32	9	US-09-843-221A-31	Sequence 31, Appli

## ALIGNMENTS

```
RESULT 1
US-09-928-047B-1
; Sequence 1, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928.047B
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-1

Query Match      100.0%; Score 422; DB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VSEIQLMHLGKHLNSMERVETLRKKLDVHNFFALGAPLRDAGSORPRKKEDNVIVE 60
DB      1 VSEIQLMHLGKHLNSMERVETLRKKLDVHNFFALGAPLRDAGSORPRKKEDNVIVE 60
QY      61 SHEKSLGEANKADVNLTKAKSQ 83
DB      61 SHEKSLGEANKADVNLTKAKSQ 83

RESULT 2
US-09-928-047B-5
; Sequence 5, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
```

FILE REFERENCE: 53221-20002.00  
CURRENT APPLICATION NUMBER: US/09/928,047B  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: US 60/224,446  
PRIOR FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 84  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-928-047B-5

Query Match 100.0%; Score 422; DB 9; Length 84;  
Best Local Similarity 100.0%; Pred. No. 1.1e-42;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMEREWLRRKKLDYHNFVALGAPLAPRDAGSORPRKKEDNVLYE 60  
DB 2 VSEIQLMHNIGKHLNSMEREWLRRKKLDYHNFVALGAPLAPRDAGSORPRKKEDNVLYE 61

QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
DB 62 SHEKSLGEANKADVNVLTAKSQ 84

## RESULT 3

US-09-928-047B-2  
Sequence 2, Application US/09928047B  
Patent No. US20020160945A1  
GENERAL INFORMATION:  
APPLICANT: Cantor, Thomas  
TITLE OF INVENTION: CYCLASE INHIBITTING PARATHYROID HORMONE  
FILE REFERENCE: 53221-20002.00  
CURRENT APPLICATION NUMBER: US/09/928,047B  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: US 60/224,446  
PRIOR FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 82  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-928-047B-2

Query Match 99.1%; Score 418; DB 9; Length 82;  
Best Local Similarity 100.0%; Pred. No. 3.2e-42;  
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEIQLMHNIGKHLNSMEREWLRRKKLDYHNFVALGAPLAPRDAGSORPRKKEDNVLYE 61  
DB 1 SEIQLMHNIGKHLNSMEREWLRRKKLDYHNFVALGAPLAPRDAGSORPRKKEDNVLYE 60

QY 62 HEKSLGEANKADVNVLTAKSQ 83  
DB 61 HEKSLGEANKADVNVLTAKSQ 82

## RESULT 4

US-09-843-221A-10  
Sequence 10, Application US/09843221A  
Patent No. US20030039654A1  
GENERAL INFORMATION:  
APPLICANT: KOSTENIUK, PAUL  
APPLICANT: LIU, CHUAN-FA  
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
FILE REFERENCE: A-665B  
CURRENT APPLICATION NUMBER: US/09/843,221A  
CURRENT FILING DATE: 2001-04-26

PRIOR APPLICATION NUMBER: 60/266,673  
PRIOR FILING DATE: 2001-02-06  
PRIOR APPLICATION NUMBER: 60/214,860  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/200,053  
PRIOR FILING DATE: 2000-04-27  
NUMBER OF SEQ ID NOS: 170  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 84  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-843-221A-10

Query Match 98.8%; Score 417; DB 9; Length 84;  
Best Local Similarity 98.8%; Pred. No. 4.3e-42;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMEREWLRRKKLDYHNFVALGAPLAPRDAGSORPRKKEDNVLYE 60  
DB 2 VSEIQLMHNIGKHLNSMEREWLRRKKLDYHNFVALGAPLAPRDAGSORPRKKEDNVLYE 61

QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
DB 62 SHEKSLGEANKADVNVLTAKSQ 84

## RESULT 5

US-09-169-786-1  
Sequence 1, Application US/09169786B  
Patent No. US20020025929A1  
GENERAL INFORMATION:  
APPLICANT: Sato, Masahiko  
TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE  
FILE REFERENCE: X-11480  
CURRENT APPLICATION NUMBER: US/09/169,786B  
CURRENT FILING DATE: 1998-10-09  
EARLIER APPLICATION NUMBER: US 60/061,800  
EARLIER FILING DATE: 1997-10-14  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 84  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-169-786-1

Query Match 98.8%; Score 417; DB 10; Length 84;  
Best Local Similarity 98.8%; Pred. No. 4.3e-42;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMEREWLRRKKLDYHNFVALGAPLAPRDAGSORPRKKEDNVLYE 60  
DB 2 VSEIQLMHNIGKHLNSMEREWLRRKKLDYHNFVALGAPLAPRDAGSORPRKKEDNVLYE 61

QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
DB 62 SHEKSLGEANKADVNVLTAKSQ 84

## RESULT 6

US-09-928-047B-4  
Sequence 4, Application US/09928047B  
Patent No. US20020160945A1  
GENERAL INFORMATION:  
APPLICANT: Cantor, Thomas  
TITLE OF INVENTION: CYCLASE INHIBITTING PARATHYROID HORMONE  
FILE REFERENCE: 53221-20002.00  
CURRENT APPLICATION NUMBER: US/09/928,047B  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: US 60/224,446  
PRIOR FILING DATE: 2000-08-10



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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 78
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-928-047B-4
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Query Match          94.8%; Score 400; DB 9; Length 78;
Best Local Similarity 100.0%; Pred. No. 3.9e-40;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 LMHNIGKHLNSMERVWMLKKLDVHNFFVALGAPLAPRDAGSQRPKKEDNVLVESHERS 65
DB 1 LMHNIGKHLNSMERVWMLKKLDVHNFFVALGAPLAPRDAGSQRPKKEDNVLVESHERS 60
QY 66 LGEANKADVNVLTAKSQ 83
DB 61 LGEANKADVNVLTAKSQ 78
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## RESULT 7

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US-09-843-221A-12
; Sequence 12, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENJIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 78
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-843-221A-12
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Best Local Similarity 98.7%; Pred. No. 1.5e-39;
Matches 77; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 LMHNIGKHLNSMERVWMLKKLDVHNFFVALGAPLAPRDAGSQRPKKEDNVLVESHERS 60
QY 66 LGEANKADVNVLTAKSQ 83
DB 61 LGEANKADVNVLTAKSQ 78
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## RESULT 8

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US-09-879-257A-49
; Sequence 49, Application US/09879257A
; Patent No. US20020081690A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIKO
; APPLICANT: HANADA, TOSHIRO
; APPLICANT: SHIRO, MINORU
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
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```
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 84
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-879-257A-49
```

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Query Match          85.1%; Score 359; DB 10; Length 84;
Best Local Similarity 85.5%; Pred. No. 2.8e-35;
Matches 71; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
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```
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DB 2 VSEIQLMHNLGKHLNSMERVWMLKKLDVHNFFVALGAPLAPRDAGSQRPKKEDNVLV 61
QY 61 SHEKSLGEANKADVNVLTAKSQ 83
DB 62 SHEKSLGEANKADVNVLTAKSQ 84
```

## RESULT 9

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US-09-843-221A-11
; Sequence 11, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENJIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROI
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 84
; TYPE: prt
; ORGANISM: Rattus rattus
US-09-843-221A-11
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Query Match          74.6%; Score 315; DB 9; Length 84;
Best Local Similarity 73.5%; Pred. No. 4.1e-30;
Matches 61; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
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QY 1 VSEIQLMHNLGKHLNSMERVWMLKKLDVHNFFVALGAPLAPRDAGSQRPKKEDNVLV 60
DB 2 VSEIQLMHNLGKHLNSMERVWMLKKLDVHNFFVALGAPLAPRDAGSQRPKKEDNVLV 61
QY 61 SHEKSLGEANKADVNVLTAKSQ 83
DB 62 SHEKSLGEANKADVNVLTAKSQ 84
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## RESULT 10

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US-09-928-047B-8
; Sequence 8, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
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;; PRIOR APPLICATION NUMBER: US 60/224,446  
;; PRIOR FILING DATE: 2000-08-10  
;; NUMBER OF SEQ ID NOS: 8  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 8  
;; LENGTH: 57  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-928-047B-8

Query Match 67.8%; Score 286; DB 9; Length 57;  
Best Local Similarity 100.0%; Pred. No. 6.6e-27;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LDVHNEVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 83  
Db 1 LDVHNEVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 57

RESULT 11  
US-09-928-047B-3  
; Sequence 3, Application US/09928047B  
; Patent No. US20020160945A1  
; GENERAL INFORMATION:  
; APPLICANT: Cantor, Thomas  
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE  
; FILE REFERENCE: 53221-20002.00  
; CURRENT APPLICATION NUMBER: US/09/928,047B  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/224,446  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-928-047B-3

Query Match 60.0%; Score 253; DB 9; Length 51;  
Best Local Similarity 100.0%; Pred. No. 4.3e-23;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 FVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 83  
Db 1 FVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51

RESULT 12  
US-09-928-047B-7  
; Sequence 7, Application US/09928047B  
; Patent No. US20020160945A1  
; GENERAL INFORMATION:  
; APPLICANT: Cantor, Thomas  
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE  
; FILE REFERENCE: 53221-20002.00  
; CURRENT APPLICATION NUMBER: US/09/928,047B  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/224,446  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 50  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-928-047B-7

Query Match 58.5%; Score 247; DB 9; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.2e-22;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 VALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 83  
Db 1 VALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 50

RESULT 13  
US-09-843-221A-13  
; Sequence 13, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENIUK, PAUL  
; APPLICANT: LIU, CHUAN-PA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; PRIOR FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-843-221A-13

Query Match 53.1%; Score 224; DB 9; Length 44;  
Best Local Similarity 100.0%; Pred. No. 9.3e-20;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMERVEMLRKKLDVHNEVALGAPLAPR 43  
Db 2 VSEIQLMHNIGKHLNSMERVEMLRKKLDVHNEVALGAPLAPR 44

RESULT 14  
US-09-843-221A-15  
; Sequence 15, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENIUK, PAUL  
; APPLICANT: LIU, CHUAN-PA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; PRIOR FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-843-221A-15

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Best Local Similarity 100.0%; Pred. No. 3.3e-16;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMERVEWLRKKLDVHNFFVALG 37  
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DB 1 VSEIQLMHNIGKHLNSMERVEWLRKKLDVHNFFVALG 37

## RESULT 15

US-09-843-221A-14  
; Sequence 14, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENDIJK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-843-221A-14

Query Match 45.7%; Score 193; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 3.4e-16;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VSEIQLMHNIGKHLNSMERVEWLRKKLDVHNFFVALG 37  
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DB 2 VSEIQLMHNIGKHLNSMERVEWLRKKLDVHNFFVALG 38

Search completed: March 13, 2003, 14:59:13  
Job time : 14.6269 secs

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OM protein - protein search, using sw model

Run on: March 13, 2003, 14:51:54 ; Search time 8.3713 Seconds  
(without alignments)  
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Title: US-09-636-530-3  
Perfect score: 253  
Sequence: 1 FVALGAPLAPRDAGSQRPKR.....KSLGEANKADVNLTKAKSQ 51

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Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

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11: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	253	100.0	57	9	US-09-928-047B-8
3	253	100.0	78	9	US-09-928-047B-4
4	253	100.0	82	9	US-09-928-047B-2
5	253	100.0	83	9	US-09-928-047B-1
6	253	100.0	84	9	US-09-928-047B-5
7	248	98.0	78	9	US-09-843-221A-12
8	248	98.0	84	9	US-09-843-221A-10
9	248	98.0	84	10	US-09-169-786-1
10	247	97.6	50	9	US-09-928-047B-7
11	199	78.7	84	10	US-09-879-257A-49
12	164	64.8	84	9	US-09-843-221A-11
13	61	24.1	557	10	US-09-815-242-12165
14	61	24.1	557	10	US-09-815-242-5464
15	59	23.3	557	10	US-09-815-242-12804
16	57	22.5	238	10	US-09-323-998B-41
17	55.5	21.9	46	10	US-09-864-761-34138
18	55	21.7	44	9	US-09-843-221A-13
19	55	21.7	1157	10	US-09-935-291A-12

20	55	21.7	1518	10	US-09-801-368-152	Sequence 152, App
21	54	21.3	1033	9	US-09-820-843A-75	Sequence 75, Appl
22	52	20.6	133	10	US-09-765-272-188	Sequence 188, App
23	52	20.6	287	10	US-09-323-998B-17	Sequence 17, Appl
24	52	20.6	682	10	US-09-815-242-11214	Sequence 11214, A
25	51.5	20.4	797	10	US-09-815-242-4882	Sequence 4882, Ap
26	51.5	20.4	798	10	US-09-815-242-10764	Sequence 10764, A
27	51	20.2	307	10	US-09-323-998B-45	Sequence 45, Appl
28	51	20.2	2308	12	US-10-000-954-2	Sequence 2, Appl
29	50.5	20.0	318	9	US-09-738-626-4032	Sequence 4032, Ap
30	50.5	20.0	591	10	US-09-764-864-1139	Sequence 1139, Ap
31	50.5	20.0	596	10	US-09-797-039-8	Sequence 8, Appl
32	50.5	20.0	602	9	US-10-121-235-19	Sequence 19, Appl
33	50.5	20.0	739	9	US-10-160-663-2	Sequence 2, Appl
34	50.5	20.0	1051	9	US-09-976-059-13	Sequence 13, Appl
35	50	19.8	592	10	US-09-797-862-2	Sequence 2, Appl
36	50	19.8	913	10	US-09-848-294-2	Sequence 2, Appl
37	50	19.8	1464	9	US-09-842-777-10	Sequence 10, Appl
38	49.5	19.6	243	9	US-09-746-783-210	Sequence 210, App
39	49.5	19.6	491	9	US-09-853-257-2	Sequence 2, Appl
40	49.5	19.6	655	9	US-09-738-626-4563	Sequence 4563, Ap
41	49.5	19.6	1616	9	US-09-820-843A-16	Sequence 16, Appl
42	49	19.4	141	9	US-09-764-868-1046	Sequence 1046, Ap
43	49	19.4	172	10	US-09-734-017A-2	Sequence 2, Appl
44	49	19.4	184	10	US-09-764-864-1280	Sequence 1280, Ap
45	49	19.4	238	9	US-09-738-626-4368	Sequence 4368, Ap

#### ALIGNMENTS

RESULT 1  
US-09-928-047B-3  
Sequence 3, Application US/09928047B  
Patent No. US20020160945A1  
GENERAL INFORMATION:  
APPLICANT: Cantor, Thomas  
TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE  
FILE REFERENCE: 53221-20002.00  
CURRENT APPLICATION NUMBER: US/09/928-047B  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: US 60/224,446  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 51  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-928-047B-3

Query Match 100.0%; Score 253; DB 9; Length 51;  
Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKRKKEDNVLSHEKSLGEANKADVNLTKAKSQ 51  
DB 1 FVALGAPLAPRDAGSQRPKRKKEDNVLSHEKSLGEANKADVNLTKAKSQ 51

RESULT 2  
US-09-928-047B-8  
Sequence 8, Application US/09928047B  
Patent No. US20020160945A1  
GENERAL INFORMATION:  
APPLICANT: Cantor, Thomas  
TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE  
FILE REFERENCE: 53221-20002.00  
CURRENT APPLICATION NUMBER: US/09/928-047B  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: US 60/224,446

;; PRIOR FILING DATE: 2000-08-10  
;; NUMBER OF SEQ ID NOS: 8  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 8  
;; LENGTH: 57  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-928-047B-8

Query Match 100.0%; Score 253; DB 9; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3.7e-26;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
DB 7 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 57

## RESULT 3

US-09-928-047B-4  
; Sequence 4, Application US/09928047B  
; Patent No. US20020160945A1  
; GENERAL INFORMATION:  
; APPLICANT: Cantor, Thomas  
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE  
; FILE REFERENCE: 53221-20002.00  
; CURRENT APPLICATION NUMBER: US/09/928,047B  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/224,446  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 78  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-928-047B-4

Query Match 100.0%; Score 253; DB 9; Length 78;  
Best Local Similarity 100.0%; Pred. No. 5.4e-26;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
DB 28 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 78

## RESULT 4

US-09-928-047B-2  
; Sequence 2, Application US/09928047B  
; Patent No. US20020160945A1  
; GENERAL INFORMATION:  
; APPLICANT: Cantor, Thomas  
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE  
; FILE REFERENCE: 53221-20002.00  
; CURRENT APPLICATION NUMBER: US/09/928,047B  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/224,446  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-928-047B-2

Query Match 100.0%; Score 253; DB 9; Length 82;  
Best Local Similarity 100.0%; Pred. No. 5.8e-26;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
DB 32 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 82

## RESULT 5

US-09-928-047B-1  
; Sequence 1, Application US/09928047B  
; Patent No. US20020160945A1  
; GENERAL INFORMATION:  
; APPLICANT: Cantor, Thomas  
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE  
; FILE REFERENCE: 53221-20002.00  
; CURRENT APPLICATION NUMBER: US/09/928,047B  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/224,446  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 83  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-928-047B-1

Query Match 100.0%; Score 253; DB 9; Length 83;  
Best Local Similarity 100.0%; Pred. No. 5.9e-26;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
DB 33 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 83

## RESULT 6

US-09-928-047B-5  
; Sequence 5, Application US/09928047B  
; Patent No. US20020160945A1  
; GENERAL INFORMATION:  
; APPLICANT: Cantor, Thomas  
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE  
; FILE REFERENCE: 53221-20002.00  
; CURRENT APPLICATION NUMBER: US/09/928,047B  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/224,446  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-928-047B-5

Query Match 100.0%; Score 253; DB 9; Length 84;  
Best Local Similarity 100.0%; Pred. No. 6e-26;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
DB 34 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

## RESULT 7

US-09-843-221A-12  
; Sequence 12, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENIUK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE

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; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 12
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-12

Query Match          98.0%; Score 248; DB 9; Length 78;
Best Local Similarity 98.0%; Pred. No. 2.4e-25;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51
DB 28 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEADKADVNVLTAKSQ 78

RESULT 8
US-09-843-221A-10
; Sequence 10, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LIO, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 10
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-10

Query Match          98.0%; Score 248; DB 9; Length 84;
Best Local Similarity 98.0%; Pred. No. 2.7e-25;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51
DB 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEADKADVNVLTAKSQ 84

RESULT 9
US-09-169-786-1
; Sequence 1, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
```

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; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-1

Query Match          98.0%; Score 248; DB 10; Length 84;
Best Local Similarity 98.0%; Pred. No. 2.7e-25;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51
DB 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEADKADVNVLTAKSQ 84

RESULT 10
US-09-928-047B-7
; Sequence 7, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-7

Query Match          97.6%; Score 247; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.9e-25;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51
DB 1 VALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 50

RESULT 11
US-09-879-257A-49
; Sequence 49, Application US/09879257A
; Patent No. US20020081690A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIKO
; APPLICANT: HANADA, TOSHIRO
; APPLICANT: SHIRO, MINORU
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 49
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-257A-49

Query Match          78.7%; Score 199; DB 10; Length 84;
Best Local Similarity 80.4%; Pred. No. 6.1e-19;
```





```

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 12804
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12804

```

```

Query Match 23.3%; Score 59; DB 10; Length 557;
Best Local Similarity 31.9%; Pred. No. 9.6;
Matches 15; Conservative 11; Mismatches 17; Indels 4; Gaps 1;

```

```

QY 3 AAGATLAPRDAGSQR-----RKEDNVLYESHEKSIGENKADVNVYL 45
DB 383 AGGVSVAPVQKSSKRPARGIOKSKNAFMSQOIAKYLDKANKADIKL 429

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Search completed: March 13, 2003, 14:59:14  
 Job time : 9.37313 secs

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 13, 2003, 14:48:44 ; Search time 108.47 Seconds  
(without alignments)  
303.138 Million cell updates/sec

Title: US-09-636-530-3

Perfect score: 253

Sequence: 1 FVALGAPLAPRDAGSQRP...KSLGEANKADYVNLTKAKSQ 51

Scoring table: BLOSUM62

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/ptodata/2/paa/PCYUS.COMB.pep:\*

2: /cgn2\_6/ptodata/2/paa/US06.COMB.pep:\*

3: /cgn2\_6/ptodata/2/paa/US07.COMB.pep:\*

4: /cgn2\_6/ptodata/2/paa/US08.COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/US081.COMB.pep:\*

6: /cgn2\_6/ptodata/2/paa/US082.COMB.pep:\*

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10: /cgn2\_6/ptodata/2/paa/US086.COMB.pep:\*

11: /cgn2\_6/ptodata/2/paa/US087.COMB.pep:\*

12: /cgn2\_6/ptodata/2/paa/US088.COMB.pep:\*

13: /cgn2\_6/ptodata/2/paa/US089.COMB.pep:\*

14: /cgn2\_6/ptodata/2/paa/US090.COMB.pep:\*

15: /cgn2\_6/ptodata/2/paa/US091.COMB.pep:\*

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17: /cgn2\_6/ptodata/2/paa/US093.COMB.pep:\*

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21: /cgn2\_6/ptodata/2/paa/US097.COMB.pep:\*

22: /cgn2\_6/ptodata/2/paa/US098.COMB.pep:\*

23: /cgn2\_6/ptodata/2/paa/US099.COMB.pep:\*

24: /cgn2\_6/ptodata/2/paa/US100.COMB.pep:\*

25: /cgn2\_6/ptodata/2/paa/US101.COMB.pep:\*

26: /cgn2\_6/ptodata/2/paa/US102.COMB.pep:\*

27: /cgn2\_6/ptodata/2/paa/US60.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	253	100.0	51	US-09-323-606C-3
2	253	100.0	51	US-09-636-530-3
3	253	100.0	51	US-09-928-047B-3
4	253	100.0	51	US-09-928-048A-5
5	253	100.0	57	US-09-636-530-5
6	253	100.0	57	US-09-928-047B-8

7	253	100.0	67	US-09-323-606C-11	Sequence 11, Appl
8	253	100.0	78	US-09-323-606C-4	Sequence 4, Appl
9	253	100.0	78	US-09-928-047B-4	Sequence 4, Appl
10	253	100.0	80	US-09-323-606C-10	Sequence 10, Appl
11	253	100.0	82	US-09-323-606C-2	Sequence 2, Appl
12	253	100.0	82	US-09-636-530-4	Sequence 2, Appl
13	253	100.0	82	US-09-928-047B-2	Sequence 2, Appl
14	253	100.0	83	US-09-636-530-2	Sequence 2, Appl
15	253	100.0	83	US-09-928-047B-1	Sequence 1, Appl
16	253	100.0	83	US-09-928-048A-4	Sequence 4, Appl
17	253	100.0	84	US-09-323-606C-1	Sequence 1, Appl
18	253	100.0	84	US-09-636-530-1	Sequence 1, Appl
19	253	100.0	84	US-09-928-047B-5	Sequence 5, Appl
20	253	100.0	84	US-09-928-048A-3	Sequence 3, Appl
21	253	100.0	51	US-09-344-639D-3	Sequence 3, Appl
22	248	98.0	51	US-10-002-818-3	Sequence 3, Appl
23	248	98.0	78	US-09-231-422D-6	Sequence 6, Appl
24	248	98.0	78	US-09-344-639D-6	Sequence 6, Appl
25	248	98.0	78	US-09-843-221A-12	Sequence 12, Appl
26	248	98.0	82	US-09-344-639D-2	Sequence 2, Appl
27	248	98.0	83	US-10-002-818-2	Sequence 2, Appl
28	248	98.0	84	PCT-US02-21356-1	Sequence 1, Appl
29	248	98.0	84	PCT-US98-20848-1	Sequence 1, Appl
30	248	98.0	84	US-07-806-271-2	Sequence 2, Appl
31	248	98.0	84	US-08-016-171-2	Sequence 2, Appl
32	248	98.0	84	US-08-329-856-2	Sequence 2, Appl
33	248	98.0	84	US-08-345-151A-16	Sequence 16, Appl
34	248	98.0	84	US-08-350-530A-25	Sequence 25, Appl
35	248	98.0	84	US-08-350-709-9	Sequence 9, Appl
36	248	98.0	84	US-08-350-709B-9	Sequence 9, Appl
37	248	98.0	84	US-08-586-768-1	Sequence 1, Appl
38	248	98.0	84	US-09-169-786-1	Sequence 1, Appl
39	248	98.0	84	US-09-169-786-1	Sequence 1, Appl
40	248	98.0	84	US-09-231-422B-2	Sequence 2, Appl
41	248	98.0	84	US-09-231-422D-2	Sequence 2, Appl
42	248	98.0	84	US-09-344-639D-1	Sequence 1, Appl
43	248	98.0	84	US-09-657-276-256	Sequence 256, Appl
44	248	98.0	84	US-09-843-221A-10	Sequence 10, Appl
45	248	98.0	84	US-09-838-398-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1

US-09-323-606C-3

Sequence 3, Application US/09323606C

GENERAL INFORMATION:

APPLICANT: Cantor, Thomas

TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR

FILE REFERENCE: 53221-20009.00

CURRENT APPLICATION NUMBER: US/09/323,606C

CURRENT FILING DATE: 1999-01-18

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 51

TYPE: PRT

ORGANISM: Homo sapiens

US-09-323-606C-3

Query Match 100.0%; Score 253; DB 17; Length 51;

Best Local Similarity 100.0%; Pred. No. 7.6e-25;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRP...KSLGEANKADYVNLTKAKSQ 51

DB 1 FVALGAPLAPRDAGSQRP...KSLGEANKADYVNLTKAKSQ 51

RESULT 2

US-09-636-530-3

```
; Sequence 3, Application US/09636530
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
; FILE REFERENCE: 53221-20003.00
; CURRENT APPLICATION NUMBER: US/09/636,530
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-530-3
```

```
Query Match          100.0%; Score 253; DB 20; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
Db 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
```

```
RESULT 3
US-09-928-047B-3
; Sequence 3, Application US/09928047B
```

```
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-3
```

```
Query Match          100.0%; Score 253; DB 23; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
Db 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
```

```
RESULT 4
US-09-928-048A-5
; Sequence 5, Application US/09928048A
```

```
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-5
```

```
Query Match          100.0%; Score 253; DB 23; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.6e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
Db 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
```

```
RESULT 5
US-09-636-530-5
; Sequence 5, Application US/09636530
```

```
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
; FILE REFERENCE: 53221-20003.00
; CURRENT APPLICATION NUMBER: US/09/636,530
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-530-5
```

```
Query Match          100.0%; Score 253; DB 20; Length 57;
Best Local Similarity 100.0%; Pred. No. 8.8e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
Db 7 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 57
```

```
RESULT 6
US-09-928-047B-8
; Sequence 8, Application US/09928047B
```

```
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-8
```

```
Query Match          100.0%; Score 253; DB 23; Length 57;
Best Local Similarity 100.0%; Pred. No. 8.8e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
Db 7 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 57
```

```
RESULT 7
US-09-323-606C-11
; Sequence 11, Application US/09323606C
```

```
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
; FILE REFERENCE: 53221-20009.00
```

```

; CURRENT APPLICATION NUMBER: US/09/323,606C
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-323-606C-11

```

```

Query Match      100.0%; Score 253; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 1,1e-24;
Matches 51: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 FVALGAPLAPRDAGSQRP RKEDNVLVESHKSLGEANKADVNVLTAKSQ 51
Db 17 FVALGAPLAPRDAGSQRP RKEDNVLVESHKSLGEANKADVNVLTAKSQ 67

```

#### RESULT 8

```

US-09-323-606C-4
; Sequence 4, Application US/09323606C
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
; FILE REFERENCE: 53221-20009.00
; CURRENT APPLICATION NUMBER: US/09/323,606C
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-323-606C-4

```

```

Query Match      100.0%; Score 253; DB 17; Length 78;
Best Local Similarity 100.0%; Pred. No. 1,3e-24;
Matches 51: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 FVALGAPLAPRDAGSQRP RKEDNVLVESHKSLGEANKADVNVLTAKSQ 51
Db 28 FVALGAPLAPRDAGSQRP RKEDNVLVESHKSLGEANKADVNVLTAKSQ 78

```

#### RESULT 9

```

US-09-928-047B-4
; Sequence 4, Application US/09928047B
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-4

```

```

Query Match      100.0%; Score 253; DB 23; Length 78;
Best Local Similarity 100.0%; Pred. No. 1,3e-24;
Matches 51: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 FVALGAPLAPRDAGSQRP RKEDNVLVESHKSLGEANKADVNVLTAKSQ 51
Db 28 FVALGAPLAPRDAGSQRP RKEDNVLVESHKSLGEANKADVNVLTAKSQ 78

```

```

RESULT 10
US-09-323-606C-10
; Sequence 10, Application US/09323606C
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
; FILE REFERENCE: 53221-20009.00
; CURRENT APPLICATION NUMBER: US/09/323,606C
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-323-606C-10

```

```

Query Match      100.0%; Score 253; DB 17; Length 80;
Best Local Similarity 100.0%; Pred. No. 1,4e-24;
Matches 51: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 FVALGAPLAPRDAGSQRP RKEDNVLVESHKSLGEANKADVNVLTAKSQ 51
Db 30 FVALGAPLAPRDAGSQRP RKEDNVLVESHKSLGEANKADVNVLTAKSQ 80

```

#### RESULT 11

```

US-09-323-606C-2
; Sequence 2, Application US/09323606C
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
; FILE REFERENCE: 53221-20009.00
; CURRENT APPLICATION NUMBER: US/09/323,606C
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-323-606C-2

```

```

Query Match      100.0%; Score 253; DB 17; Length 82;
Best Local Similarity 100.0%; Pred. No. 1,4e-24;
Matches 51: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 FVALGAPLAPRDAGSQRP RKEDNVLVESHKSLGEANKADVNVLTAKSQ 51
Db 32 FVALGAPLAPRDAGSQRP RKEDNVLVESHKSLGEANKADVNVLTAKSQ 82

```

#### RESULT 12

```

US-09-636-530-4
; Sequence 4, Application US/09636530
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
; FILE REFERENCE: 53221-20003.00
; CURRENT APPLICATION NUMBER: US/09/636,530
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-530-4

```

Query Match 100.0%; Score 253; DB 20; Length 82;  
Best Local Similarity 100.0%; Pred. No. 1.4e-24;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51  
|||||  
DB 32 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 82

RESULT 13  
US-09-928-047B-2  
Sequence 2, Application US/09928047B

GENERAL INFORMATION:  
APPLICANT: Cantor, Thomas  
TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE  
TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS  
FILE REFERENCE: 53221-20002.00  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: US 60/224,446  
PRIOR FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 82  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-928-047B-2

Query Match 100.0%; Score 253; DB 23; Length 82;  
Best Local Similarity 100.0%; Pred. No. 1.4e-24;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51  
|||||  
DB 32 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 82

RESULT 14

US-09-636-530-2  
Sequence 2, Application US/09636530

GENERAL INFORMATION:  
APPLICANT: Cantor, Thomas  
TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR  
TITLE OF INVENTION: MODULATORS AND USES THEREFOR  
FILE REFERENCE: 53221-20003.00  
CURRENT APPLICATION NUMBER: US/09/636,530  
CURRENT FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 83  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-636-530-2

Query Match 100.0%; Score 253; DB 20; Length 83;  
Best Local Similarity 100.0%; Pred. No. 1.5e-24;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51  
|||||  
DB 33 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 83

RESULT 15  
US-09-928-047B-1

Sequence 1, Application US/09928047B  
GENERAL INFORMATION:  
APPLICANT: Cantor, Thomas  
TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE  
TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS

FILE REFERENCE: 53221-20002.00  
CURRENT APPLICATION NUMBER: US/09/928,047B  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: US 60/224,446  
PRIOR FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 83  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-928-047B-1

Query Match 100.0%; Score 253; DB 23; Length 83;  
Best Local Similarity 100.0%; Pred. No. 1.5e-24;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51  
|||||  
DB 33 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 83

Search completed: March 13, 2003, 14:57:47.  
Job time : 108.47 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: March 13, 2003, 14:49:19 : Search time 18.2687 seconds  
(without alignments)  
362.927 Million cell updates/sec

Title: US-09-636-530-3

Sequence: 1 FVALGAPLAPRDAGSQRRPK.....KSLGEANKADVNLTKAKSQ 51

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	253	100.0	78	5	US-09-231-422F-6
2	253	100.0	84	1	PCT-US02-25348-1
3	253	100.0	84	5	US-09-231-422F-2
4	253	100.0	84	6	US-10-215-770-1
5	248	98.0	84	1	PCT-US02-40891-505
6	248	98.0	84	1	PCT-US02-40891-508
7	248	98.0	84	1	PCT-US02-40891-530
8	248	98.0	84	1	PCT-US02-40891-531
9	248	98.0	84	1	PCT-US02-40891-532
10	248	98.0	84	1	PCT-US02-40891-626
11	248	98.0	84	1	PCT-US03-02155-13
12	248	98.0	84	5	US-09-383-590-1
13	248	98.0	84	6	US-10-224-522-1
14	248	98.0	84	6	US-10-311-366-10
15	248	98.0	692	1	PCT-US02-40891-289
16	248	98.0	692	1	PCT-US02-40891-292
17	248	98.0	693	1	PCT-US02-40891-314
18	248	98.0	693	1	PCT-US02-40891-315
19	248	98.0	693	1	PCT-US02-40891-316
20	248	98.0	693	1	PCT-US02-40891-316
21	206	81.4	84	3	PCT-US02-25348-3
22	206	81.4	84	6	US-10-215-770-3
23	199	78.7	84	1	PCT-US02-25348-4
24	199	78.7	84	6	US-10-311-366-2
25	199	78.7	84	6	US-10-215-770-4
26	194	76.7	84	1	PCT-US02-25348-2

27	194	76.7	84	6	US-10-215-770-2	Sequence 2, Appl
28	164	64.8	84	6	US-10-311-366-11	Sequence 11, Appl
29	160	63.2	84	1	PCT-US02-25348-5	Sequence 5, Appl
30	160	63.2	84	6	US-10-215-770-5	Sequence 5, Appl
31	151	59.7	32	6	US-10-311-366-27	Sequence 27, Appl
32	97	38.3	22	6	US-10-311-366-3	Sequence 3, Appl
33	95	37.5	21	6	US-10-311-366-4	Sequence 4, Appl
34	84	33.2	91	7	US-60-443-566-2959	Sequence 2959, Ap
35	84	33.2	123	7	US-60-443-566-2960	Sequence 2960, Ap
36	75	29.6	21	6	US-10-311-366-26	Sequence 26, Appl
37	75	29.6	22	6	US-10-311-366-25	Sequence 25, Appl
38	68.5	27.1	88	1	PCT-US02-25348-6	Sequence 6, Appl
39	68.5	27.1	88	6	US-10-215-770-6	Sequence 6, Appl
40	66	26.1	15	6	US-10-311-366-6	Sequence 6, Appl
41	66	26.1	15	6	US-10-311-366-5	Sequence 5, Appl
42	61	24.1	565	6	US-10-282-122A-43871	Sequence 43871, A
43	61	24.1	566	6	US-10-282-287-4	Sequence 4, Appl
44	60	23.7	1942	6	US-10-144-779-422	Sequence 422, App
45	59	23.3	130	1	PCT-US02-32727-13961	Sequence 13961, A

## ALIGNMENTS

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RESULT 1
US-09-231-422F-6
; Sequence 6, Application US/09231422F
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas
; APPLICANT: Gao, Ping
; TITLE OF INVENTION: METHODS, KITS AND ANTIBODIES FOR DETECTING
; TITLE OF INVENTION: PARATHYROID HORMONE
; FILE REFERENCE: 53221-20006.00
; CURRENT APPLICATION NUMBER: US/09/231,422F
; CURRENT FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-231-422F-6

Query Match      100.0%; Score 253; DB 5; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.8e-22;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      28 FVALGAPLAPRDAGSQRRPKEDNVLVESHEKSLGEANKADVNLTKAKSQ 78

RESULT 2
PCT-US02-25348-1
; Sequence 1, Application PC/TUS0225348
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
; FILE REFERENCE: 53221-20002.40
; CURRENT APPLICATION NUMBER: PCT/US02/25348
; CURRENT FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-25348-1

Query Match      100.0%; Score 253; DB 1; Length 84;
Best Local Similarity 100.0%; Pred. No. 2e-22;

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Matches 51: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
|||||  
Db 34 FVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

RESULT 3  
US-09-231-422F-2  
; Sequence 2, Application US/09231422F  
; GENERAL INFORMATION:  
; APPLICANT: Scantibodies Laboratory, Inc.  
; APPLICANT: Cantor, Thomas  
; APPLICANT: Gao, Ping  
; TITLE OF INVENTION: METHODS, KITS AND ANTIBODIES FOR DETECTING  
; TITLE OF INVENTION: PARATHYROID HORMONE  
; FILE REFERENCE: 53221-20006.00  
; CURRENT APPLICATION NUMBER: US/09/231,422F  
; CURRENT FILING DATE: 1999-01-14  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-231-422F-2

Query Match 100.0%; Score 253; DB 5; Length 84;  
Best Local Similarity 100.0%; Pred. No. 2e-22;  
Matches 51: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
|||||  
Db 34 FVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

RESULT 4  
US-10-215-770-1  
; Sequence 1, Application US/10215770  
; GENERAL INFORMATION:  
; APPLICANT: Cantor, Thomas L.  
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 53221-20002.20  
; CURRENT APPLICATION NUMBER: US/10/215,770  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: US 60/224,446  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: US 60/224,447  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-215-770-1

Query Match 100.0%; Score 253; DB 6; Length 84;  
Best Local Similarity 100.0%; Pred. No. 2e-22;  
Matches 51: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
|||||  
Db 34 FVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

RESULT 5  
PCT-US02-40891-505  
; Sequence 505, Application PC/TUS0240891  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PFS64PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/40891  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 60/341,811  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/360,000  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 60/378,950  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/398,008  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: 60/411,355  
; PRIOR FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/414,984  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: 60/417,611  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/420,246  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: 60/423,623  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/351,360  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2222  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 505  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-40891-505

Query Match 98.0%; Score 248; DB 1; Length 84;  
Best Local Similarity 98.0%; Pred. No. 7.7e-22;  
Matches 50: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51  
|||||  
Db 34 FVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

RESULT 6  
PCT-US02-40891-508  
; Sequence 508, Application PC/TUS0240891  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PFS64PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/40891  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 60/341,811  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/360,000  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 60/378,950  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/398,008  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: 60/411,355  
; PRIOR FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/414,984  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: 60/417,611  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/420,246  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: 60/423,623  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/351,360  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2222  
; SOFTWARE: PatentIn Ver. 2.0



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; SEQ ID NO 508
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-40891-508
```

```
Query Match          98.0%; Score 248; DB 1; Length 84;
Best Local Similarity 98.0%; Pred. No. 7.7e-22;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHESLSGEANKADVNVLTAKSQ 51
Db 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHESLSGEADKADVNVLTAKSQ 84
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```
RESULT 7
PCT-US02-40891-530
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; Sequence 530, Application PC/TUS0240891
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564PCT
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 530
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-40891-530
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Query Match          98.0%; Score 248; DB 1; Length 84;
Best Local Similarity 98.0%; Pred. No. 7.7e-22;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHESLSGEANKADVNVLTAKSQ 51
Db 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHESLSGEADKADVNVLTAKSQ 84
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RESULT 8
PCT-US02-40891-531
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; Sequence 531, Application PC/TUS0240891
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564PCT
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
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; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 531
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-40891-531
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Query Match          98.0%; Score 248; DB 1; Length 84;
Best Local Similarity 98.0%; Pred. No. 7.7e-22;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHESLSGEANKADVNVLTAKSQ 51
Db 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHESLSGEADKADVNVLTAKSQ 84
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RESULT 9
PCT-US02-40891-532
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; Sequence 532, Application PC/TUS0240891
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564PCT
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 532
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-40891-532
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Query Match 98.0%; Score 248; DB 1; Length 84;  
Best Local Similarity 98.0%; Pred. No. 7.7e-22;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51  
DB 34 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEADKADVNVLTAKSQ 84

## RESULT 10

PCT-US02-40891-626

; Sequence 626, Application PC/TUS0240891  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: P564PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/40891  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 60/341,811  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/360,000  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 60/378,950  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/398,008  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: 60/411,355  
; PRIOR FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/414,984  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: 60/417,611  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/420,246  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: 60/423,623  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/351,360  
; PRIOR FILING DATE: 2002-01-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2222  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 626  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens

PCT-US02-40891-626

Query Match 98.0%; Score 248; DB 1; Length 84;  
Best Local Similarity 98.0%; Pred. No. 7.7e-22;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51  
DB 34 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEADKADVNVLTAKSQ 84

## RESULT 11

PCT-US03-02155-13

; Sequence 13, Application PC/TUS0302155  
; GENERAL INFORMATION:  
; APPLICANT: Gardella, Thomas J.  
; APPLICANT: Kronenberg, Henry M.  
; APPLICANT: Potts, John T.  
; TITLE OF INVENTION: Conformationally Constrained Parathyroid Hormone (PTH) Analogs  
; FILE REFERENCE: 0609,514PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/02155  
; CURRENT FILING DATE: 2003-01-24  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Version 3.2  
; SEQ ID NO 13  
; LENGTH: 84

; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (84)..(84)  
; OTHER INFORMATION: AMIDATION  
PCT-US03-02155-13

Query Match 98.0%; Score 248; DB 1; Length 84;  
Best Local Similarity 98.0%; Pred. No. 7.7e-22;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51  
DB 34 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEADKADVNVLTAKSQ 84

## RESULT 12

US-09-383-590-1

; Sequence 1, Application US/09383590  
; GENERAL INFORMATION:  
; APPLICANT: Backstrom, Kjell G. E.  
; APPLICANT: Wallmark, Bjorn  
; APPLICANT: Dahlback, Magnus  
; APPLICANT: Edman, Peter  
; APPLICANT: Johansson, Ann  
; TITLE OF INVENTION: THERAPEUTIC PREPARATIONS FOR INHALATION  
; FILE REFERENCE: 06275-110002  
; CURRENT APPLICATION NUMBER: US/09/383,590  
; CURRENT FILING DATE: 1999-08-26  
; PRIOR APPLICATION NUMBER: US 08/586,768  
; PRIOR FILING DATE: 1996-01-30  
; PRIOR APPLICATION NUMBER: PCT/SE95/01475  
; PRIOR FILING DATE: 1995-12-08  
; PRIOR APPLICATION NUMBER: SE 9404449-2  
; PRIOR FILING DATE: 1994-12-22  
; PRIOR APPLICATION NUMBER: SE 9502576-3  
; PRIOR FILING DATE: 1995-07-12  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-383-590-1

Query Match 98.0%; Score 248; DB 5; Length 84;  
Best Local Similarity 98.0%; Pred. No. 7.7e-22;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51  
DB 34 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEADKADVNVLTAKSQ 84

## RESULT 13

US-10-224-522-1

; Sequence 1, Application US/10224522  
; GENERAL INFORMATION:  
; APPLICANT: Backstrom, Kjell G. E.  
; APPLICANT: Wallmark, Bjorn  
; APPLICANT: Dahlback, Magnus  
; APPLICANT: Edman, Peter  
; APPLICANT: Johansson, Ann  
; TITLE OF INVENTION: THERAPEUTIC PREPARATIONS FOR INHALATION  
; FILE REFERENCE: 06275-110003  
; CURRENT APPLICATION NUMBER: US/10/224,522  
; CURRENT FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 09/383,590  
; PRIOR FILING DATE: 1999-08-26  
; PRIOR APPLICATION NUMBER: US 08/586,768  
; PRIOR FILING DATE: 1996-01-30  
; PRIOR APPLICATION NUMBER: PCT/SE95/01475

; PRIOR FILING DATE: 1995-12-08  
; PRIOR APPLICATION NUMBER: SE 9404449-2  
; PRIOR FILING DATE: 1994-12-22  
; PRIOR APPLICATION NUMBER: SE 9502576-3  
; PRIOR FILING DATE: 1995-07-12  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-224-522-1

Query Match 98.0%; Score 248; DB 6; Length 84;  
Best Local Similarity 98.0%; Pred. No. 7.7e-22;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51  
Db 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEADKADVNVLTAKSQ 84

RESULT 14  
US-10-311-366-10  
; Sequence 10, Application US/10311366  
; GENERAL INFORMATION:  
; APPLICANT: Hollick, Michael F.  
; TITLE OF INVENTION: Regulation Of Cell Proliferation And Differentiation Using Topica  
; FILE REFERENCE: 1539.0310001  
; CURRENT APPLICATION NUMBER: US/10/311.366  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: PCT/US01/19650  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: US 60/213.247  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: hPTH  
US-10-311-366-10

Query Match 98.0%; Score 248; DB 6; Length 84;  
Best Local Similarity 98.0%; Pred. No. 7.7e-22;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51  
Db 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEADKADVNVLTAKSQ 84

RESULT 15  
PCT-US02-40891-289  
; Sequence 289, Application PC/TUS0240891  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PFS6APCT  
; CURRENT APPLICATION NUMBER: PCT/US02/40891  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 60/341,811  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/360,000  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 60/378,950  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/398,008  
; PRIOR FILING DATE: 2002-07-24

; PRIOR APPLICATION NUMBER: 60/411,355  
; PRIOR FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/414,984  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: 60/417,611  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/420,246  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: 60/423,623  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/351,360  
; PRIOR FILING DATE: 2002-01-28  
; Remaining Prior Application data removed - See file Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2222  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 289  
; LENGTH: 692  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (532)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
PCT-US02-40891-289

Query Match 98.0%; Score 248; DB 1; Length 692;  
Best Local Similarity 98.0%; Pred. No. 8e-21; Indels 0; Gaps 0;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51  
Db 642 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEADKADVNVLTAKSQ 692

Search completed: March 13, 2003, 14:58:43  
Job time : 18.2687 secs

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OM protein - protein search, using sw model

Run on: March 13, 2003, 14:58:49 ; Search time 9.89552 Seconds  
(without alignments) 495.462 Million cell updates/sec

Title: US-09-636-530-3  
Perfect score: 253  
Sequence: 1 FVALGAPLAPFDAGSQRRK.....KSLGEANKADVNLTKAKSQ 51

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR\_73:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	98.0	115	1	PTHU
2	206	81.4	115	2	UC4202
3	199	78.7	115	1	PTHU
4	194	76.7	115	1	PTHU
5	160	63.2	105	2	IS1851
6	160	63.2	115	2	A05091
7	68.5	27.1	119	2	A34937
8	65	25.7	283	2	H86803
9	63.5	25.1	487	2	A11407
10	63	24.9	1937	2	I38055
11	61.5	24.3	366	2	A64028
12	61	24.1	565	2	G89813
13	60.5	23.9	555	2	T44010
14	60	23.7	258	2	A02985
15	60	23.7	955	2	S24348
16	60	23.7	1938	2	A59293
17	60	23.7	1940	2	A29320
18	60	23.7	5170	2	T15348
19	59.5	23.5	1400	2	T33758
20	59	23.3	404	2	C64597
21	58.5	23.1	142	2	T45922
22	58	22.9	234	2	S33732
23	58	22.9	465	2	A02986
24	58	22.9	1038	1	MMRBCB
25	58	22.9	1935	1	A37102
26	58	22.9	1935	1	S06006
27	58	22.9	1935	1	A59286
28	57.5	22.7	378	2	F56533
29	56.5	22.3	655	2	C71438

30	56.5	22.3	674	2	B71438	hypothetical prote
31	56.5	22.3	727	2	T24284	hypothetical prote
32	56	22.1	396	2	G96934	DNA-damage repair
33	56	22.1	1787	2	G97222	hypothetical prote
34	56	22.1	1931	2	A59234	slow myosin heavy
35	56	22.1	1938	1	JX0178	myosin heavy chain
36	55.5	21.9	412	2	T51080	hypothetical prote
37	55.5	21.9	1203	2	S26550	DNA-binding protei
38	55	21.7	269	2	T15500	hypothetical prote
39	55	21.7	854	2	S02003	neurofilament trip
40	55	21.7	1072	1	A37221	neurofilament trip
41	55	21.7	1154	2	T18525	diacylglycerol kin
42	55	21.7	1157	2	T19187	hypothetical prote
43	55	21.7	1505	2	T31418	synapcomomal compl
44	55	21.7	1518	2	S37928	probable purine nu
45	55	21.7	1934	2	I48153	myosin heavy chain

## ALIGNMENTS

RESULT 1  
PTHU  
parathyroid hormone precursor [validated] - human  
N:Alternate names: proparathyroid hormone  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence\_revision 19-Jan-1996 #text\_change 08-Dec-2000  
C:Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90287; A90426; A94410;  
R:Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr.  
Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983  
A:Title: Nucleotide sequence of the human parathyroid hormone gene.  
A:Reference number: A19339; MUID:83169834; PMID:6220408  
A:Accession: A19339  
A:Molecule type: DNA  
A:Residues: 1-115 <VAS>  
A:Cross-references: GB:J00301; MID:9190702; PIDN:AAA60215.1; PID:9190704  
R:Yamauchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.  
Biol. Chem. Hoppe-Seyler 375, 821-824, 1994  
A:Title: Purification of meprin from human kidney and its role in parathyroid hormone  
A:Reference number: S53790; MUID:95225988; PMID:7710697  
A:Accession: S53790  
A:Molecule type: Protein  
A:Residues: 'X',33,'X',35-46;65-84;105-110 <YAM>  
A>Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occu  
R:Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.  
Nature 249, 155-157, 1974  
A:Title: Structural analysis of human parathyroid hormone by a new microsequencing  
A:Reference number: A93169; MUID:74174967; PMID:4833516  
A:Accession: A93169  
A:Molecule type: protein  
A:Residues: 26-37 <JAC>  
R:Olstead, O.K.; Røpke, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik,  
Eur. J. Biochem. 205, 311-319, 1992  
A:Title: Isolation and characterization of two biologically active O-glycosylated for  
A:Reference number: S21199; MUID:92209518; PMID:1555591  
A:Accession: S21199  
A:Molecule type: protein  
A:Residues: 32-114,'N' <OLS>  
A>Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylati  
R:Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L  
Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974  
A:Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyro  
A:Reference number: A93789; MUID:74111656; PMID:4521809  
A:Accession: A93789  
A:Molecule type: protein  
A:Residues: 32-68 <NIA>  
R:Brewer Jr., H.B.; Fairwell, T.; Roman, R.; Sizemore, G.W.; Arnaud, C.D.  
Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972  
A:Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residue  
A:Reference number: A93783; MUID:73070429; PMID:4509319  
A:Accession: A93783  
A:Molecule type: protein

A:Residues: 32-52, 'Q', 54-58, 'K', 60, 'L', 62-65 <BRE>  
A:Note: this sequence was determined by sequenator and mass spectroscopic identification  
R:Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.  
Biochemistry 14, 1842-1847, 1975  
A:Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.  
A:Reference number: A90387; MUID:75146516; PMID:1125201  
A:Accession: A90387  
A:Molecule type: protein  
A:Residues: 52-75 <KE3>  
R:Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.  
Biochemistry 17, 5723-5729, 1978  
A:Title: Complete amino acid sequence of human parathyroid hormone.  
A:Reference number: A90426; MUID:79082855; PMID:728431  
A:Accession: A90426  
A:Molecule type: protein  
A:Residues: 61-106, 'D', 108-115 <KEU>  
R:Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.  
In Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-  
A:Reference number: A94410  
A:Accession: A94410  
A:Molecule type: protein  
A:Residues: 75-100 <KE2>  
R:Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J.  
Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974  
A:Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of hum  
A:Reference number: A91660; MUID:75059220; PMID:4474131  
A:Contents: annotation; synthesis of residues 32-65  
A:Note: the biologically active amino-terminal 34 residues of parathyroid hormone were s  
at renal adenylate cyclase assay and with the bovine hormone's active region in the chi  
R:Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Walter, R.; Rittler, B.; Rittler,  
Heiv. Chim. Acta 56, 470-473, 1973  
A:Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.  
A:Reference number: A91635; MUID:73227467; PMID:4721748  
A:Contents: annotation; synthesis of residues 32-65  
A:Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined  
into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level  
R:Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981  
A:Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.  
A:Reference number: I38342; MUID:82150870; PMID:6950381  
A:Accession: I38342  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <RES>  
A:Cross-references: EMBL:V00597; NID:g37143; PIDN:CAA23843.1; PID:g37144  
C:Genetics:  
A:Gene: GDB:PTH  
A:Cross-references: GDB:119522; OMIM:168450  
A:Map position: 11p15.2-11p15.1  
A:Introns: 29/2  
A:Note: the first intron occurs before the initiator codon  
C:Function:  
A:Description: factor in homeostatic control of plasma calcium and phosphate: released t  
counter to calcitonin  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: calcium; hormone; parathyroid gland; plasma  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-31/Domain: propeptide #status experimental <PRO>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status experimental <MAT>  
Query Match 98.0%; Score 248; DB 1; Length 115;  
Best Local Similarity 98.0%; Pred. No. 76-23;  
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

C:Species: Canis lupus familiaris (dog)  
C:Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 16-Jul-1999  
C:Accession: Jc4202  
R:Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.  
Gene 160, 241-243, 1995  
A:Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein a  
A:Reference number: Jc4201; MUID:95369696; PMID:7642102  
A:Accession: Jc4202  
A:Molecule type: mRNA  
A:Residues: 1-115 <ROS>  
A:Cross-references: GB:U05662; NID:9558915; PIDN:AA82584.1; PID:9558916  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: hormone  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status predicted <MAT>  
Query Match 81.4%; Score 206; DB 2; Length 115;  
Best Local Similarity 82.4%; Pred. No. 8-5e-18;  
Matches 42; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

RESULT 3  
PROB  
parathyroid hormone precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 23-Oct-1981 #sequence\_revision 23-Oct-1991 #text\_change 18-Jun-1999  
C:Accession: A24949; A93835; A91648; A93773; I45975; I45976; A01534  
R:Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.  
Gene 28, 319-329, 1984  
A:Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroi  
A:Reference number: A24949; MUID:84262483; PMID:6086460  
A:Accession: A24949  
A:Molecule type: DNA  
A:Residues: 1-115 <WEA>  
A:Cross-references: GB:K01938  
R:Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr  
Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979  
A:Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid h  
A:Reference number: A93835; MUID:80056617; PMID:388425  
A:Accession: A93835  
A:Molecule type: DNA  
A:Residues: 1-115 <KRO>  
A:Cross-references: GB:U00106; GB:U00023; NID:984; PIDN:CAA23439.1; PID:985  
A:Note: the authors translated the codon GAA for residue 50 as Gly  
R:Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D  
Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974  
A:Title: The N-terminal amino-acid sequence of bovine preproparathyroid hormone.  
A:Reference number: A93793; MUID:74142666; PMID:4522780  
A:Accession: A93793  
A:Molecule type: protein  
A:Residues: 26-115 <HAM>  
R:Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; P  
Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970  
A:Title: The amino acid sequence of bovine parathyroid hormone I.  
A:Reference number: A91648; MUID:71076162; PMID:5531031  
A:Accession: A91648  
A:Molecule type: protein  
A:Residues: 32-115 <NTA>  
R:Brewer Jr., H.B.; Roman, R.  
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970  
A:Title: Bovine parathyroid hormone: amino acid sequence.  
A:Reference number: A93773; MUID:71063634; PMID:5275384  
A:Accession: A93773  
A:Molecule type: protein  
A:Residues: 32-115 <BRE>  
R:Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J  
Proc. Natl. Acad. Sci. U.S.A. 68, 65-67, 1971  
A:Title: Synthesis of a biologically active N-terminal tetrapeptide of parat

A:Reference number: A93776; MUID:71091588; PMID:4322265  
A:Residues: 32-109 <SAUV>  
A:Contents: annotation; synthesis of residues 32-65  
A>Note: the synthetic peptide was active in vivo and in vitro  
R:Breuer Jr., H.B.; Fairwell, T.; Rittell, W.; Littlelike, T.; Arnaud, C.D.  
Am. J. Med. 56, 759-766, 1974  
A>Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone  
A:Reference number: A90030; MUID:74173303; PMID:4598526  
A:Contents: annotation  
R:Weaver, C.A.; Gordon, D.F.  
Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981  
A>Title: Intracellular cloning of artificial inverted sequences at the 5' end  
A:Reference number: 145975; MUID:82037785; PMID:6170060  
A:Accession: 145975  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <ME3>  
A:CROSS-references: GB:J00024; NID:g163642; PIDN:AAA30748.1; PID:g163643  
R:Weaver, C.A.; Gordon, D.F.  
Mol. Cell. Endocrinol. 28, 411-424, 1982  
A>Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.  
A:Reference number: 145976; MUID:83105964; PMID:6185374  
A:Accession: 145976  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <ME3>  
A:CROSS-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645  
A:Residues: 1-115 <ME3>  
A:CROSS-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645  
A:Gene: PTH  
A:Introns: 29/2  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: hormone  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-115/Product: parathyroid hormone #status experimental <PMAT>  
F:26-31/Domain: propeptide #status experimental <PRO>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status experimental <MAT>  
Query Match 78.7%; Score 199; DB 1; Length 115;  
Best Local Similarity 80.4%; Pred. No. 6e-17; Mismatches 6; Indels 0; Gaps 0;  
Matches 41; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 1 FVALGAPLAPRDAGSQRPKKEDNVLESHEKSLGEANKADYVLTAKSQ 51  
DB 65 FVALGASTVNRDSSQRPKKEDNVLESHEKSLGEADKADYVLTAKPQ 115  
RESULT 4  
PPG  
parathyroid hormone precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 24-Apr-1984 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
C:Accession: B26806; A90390; A01535  
R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.  
Nucleic Acids Res. 15, 6740, 1987  
A>Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone  
A:Reference number: A26806; MUID:87316938; PMID:3628009  
A:Accession: B26806  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-115 <SCH>  
A:CROSS-references: GB:X05722; GB:Y00409; NID:g1838; PIDN:CAA29193.1; PID:g1839  
R:Chu, L.L.H.; Huang, W.Y.; Littlelike, E.T.; Hamilton, J.W.; Cohn, D.V.  
Biochemistry 14, 3631-3635, 1975  
A>Title: Porcine parathyroid hormone. Identification, biosynthesis, and partial amino acid sequence  
A:Reference number: A90390; MUID:76018954; PMID:1164500  
A:Accession: A90390  
A:Molecule type: protein  
A:Residues: 26-115 <CHU>  
R:Saner, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., J.  
Biochemistry 13, 1994-1999, 1974  
A>Title: The amino acid sequence of porcine parathyroid hormone.  
A:Reference number: A90376; MUID:74253117; PMID:4840833  
A:Accession: A90376

A:Molecule type: protein  
A:Residues: 32-109 <SAUV>  
R:Breuer Jr., H.B.; Fairwell, T.; Rittell, W.; Littlelike, T.; Arnaud, C.D.  
Am. J. Med. 56, 759-766, 1974  
A>Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone  
A:Reference number: A90030; MUID:74173303; PMID:4598526  
A:Contents: annotation  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: calcium hormone; parathyroid gland  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-31/Domain: propeptide #status experimental <PRO>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status experimental <MAT>  
Query Match 76.7%; Score 194; DB 1; Length 115;  
Best Local Similarity 78.4%; Pred. No. 2.4e-16; Mismatches 7; Indels 0; Gaps 0;  
Matches 40; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
QY 1 FVALGAPLAPRDAGSQRPKKEDNVLESHEKSLGEANKADYVLTAKSQ 51  
DB 65 FVALGASTVNRDSSQRPKKEDNVLESHEKSLGEADKADYVLTAKPQ 115  
RESULT 5  
I51851  
parathyroid hormone - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: 151851  
R:Schmelzer, H.  
Adv. Gene Technol. 21, 228-229, 1984  
A>Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.  
A:Reference number: 151851  
A:Accession: 151851  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-105 <RES>  
A:CROSS-references: GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:g601933  
A:Gene: PTH  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
F:20-54/Domain: parathyroid hormone homology <PTH>  
Query Match 63.2%; Score 160; DB 2; Length 105;  
Best Local Similarity 62.7%; Pred. No. 2.9e-12; Mismatches 11; Indels 0; Gaps 0;  
Matches 32; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
QY 1 FVALGAPLAPRDAGSQRPKKEDNVLESHEKSLGEANKADYVLTAKSQ 51  
DB 55 FVSLGVQMARAGSYQRPKKEDNVLDGNSKSLGEGDKADYVLTAKSQ 105  
RESULT 6  
A05091  
parathyroid hormone precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 16-Jul-1999  
C:Accession: A05091; A26806  
R:Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.  
J. Biol. Chem. 259, 3320-3329, 1984  
A:Reference number: A05091; MUID:84135846; PMID:6321505  
A:Accession: A05091  
A:Molecule type: DNA  
A:Residues: 1-115 <HEI>  
A:CROSS-references: GB:K01268; NID:g206483; PIDN:AAA1979.1; PID:g206485  
A>Note: the authors translated the codon GAA for residue 87 as Asp  
R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.  
Nucleic Acids Res. 15, 6740, 1987  
A>Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone  
A:Reference number: A26806; MUID:87316938; PMID:3628009  
A:Accession: A26806  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA

A:Residues: 1-115 <SCH>  
 A:Cross-references: GB:X05721; GB:Y00409; NID:956002; PIDN:CAA29192.1; PID:956003  
 C:Genetics:  
 A:Introns: 29/3  
 C:Superfamily: parathyroid hormone: parathyroid hormone homology  
 F:30-64/Domain: parathyroid hormone homology <PTH>

Query Match 63.2%; Score 160; DB 2; Length 115;  
 Best Local Similarity 62.7%; Pred. No. 3.2e-12;  
 Matches 32; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Oy 1 FVALGAPLARDAGSORPRKEDNVLYESHEKSLGEANKADVNLVTFKAKSO 51  
 Db 65 FVSLGVOMARREGSYQPTKKEKNVLVDGNSKSLGEGDKADVDVLFKAKSQ 115

RESULT 7  
 A34937

Parathyroid hormone precursor - chicken  
 C:Species: Gallus gallus (chicken)

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Jul-1999  
 C:Accession: A34937; I50411  
 R:Russell, J.; Sherwood, L.M.

Mol. Endocrinol. 3, 325-331, 1989

A:Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid  
 A:Reference number: A34937; MOID:89219100; PMID:2710135  
 A:Accession: A34937

A:Residues: 1-119 <RUS>  
 A:Molecule type: mRNA

A:Cross-references: GB:M31604; NID:g212767; PIDN:AAA9093.1; PID:g212768  
 R:Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Polls, J.T.

J. Bone Miner. Res. 3, 689-698, 1988  
 A:Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone  
 A:Reference number: I50411; MOID:89284968; PMID:3251402  
 A:Accession: I50411

A:Status: preliminary; translated from GB/EMBL/DBSJ

A:Molecule type: mRNA

A:Residues: 1-119 <RHO>

A:Cross-references: GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:g212592

C:Superfamily: parathyroid hormone: parathyroid hormone homology

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-31/Domain: propeptide #status predicted <PRO>

F:30-64/Domain: parathyroid hormone homology <PTH>

F:32-119/Product: parathyroid hormone #status predicted <MAT>

Query Match 27.1%; Score 68.5; DB 2; Length 119;  
 Best Local Similarity 38.9%; Pred. No. 0.39;  
 Matches 21; Conservative 6; Mismatches 14; Indels 13; Gaps 1;

Oy 9 APRDAGSORPRKEDNVLYE-----SHEKSLGEANKADVNLVTFKAK 49  
 Db 65 ALBDARFQRPRKEDVLYGEIRNRRLPEHLRAAVGKSIDLDKAVYNVLFKTK 118

RESULT 8  
 H86803

prophage p13 protein 59 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
 C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001

C:Accession: H86803

R:Polotkin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich  
 Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss

A:Reference number: A86625; MOID:21235186; PMID:11337471

A:Accession: H86803

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-283 <STO>

A:Cross-references: GB:AE005176; PID:g12724421; PIDN:AAK05530.1; GSPDB:GN00146

A:Experimental source: strain IL1403  
 C:Genetics:  
 A:Gene: p1359

Query Match 25.7%; Score 65; DB 2; Length 283;  
 Best Local Similarity 36.1%; Pred. No. 2.6;  
 Matches 13; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

Oy 15 SORPRKEDNVLYESHEKSLGEANKADVNLVTFKAKSO 50  
 Db 110 SKSKSDSNMLIDSOYKTELADENGADSAVLVATKS 145

RESULT 9  
 A71407

probable Ste20-like kinase - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: columbia

C:Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 16-Dec-1998

C:Accession: A71407

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D

P.; Wedler, H.; Wedler, E.; Wamulit, R.; Weitzenegeger, T.; Pohl, T.M.; Terry, N.; G

avanagh, T.; Hempel, S.; Kotler, P.; Enlitan, K.D.; Rieger, M.; Schaeffer, M.; Funk, B

Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomen

eroft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;

C.; Chalwatzis, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t

A:Reference number: A71400; MOID:98121113; PMID:9461215

A:Accession: A71407

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-487 <BEV>

A:Cross-references: GB:Z97336; NID:g2244786; PID:e326893; PID:g2244804

C:Genetics:

A:Map position: 4COP9-4G3845

C:Superfamily: protein kinase homology

F:13-293/Domain: protein kinase homology <KIN>

Query Match 25.1%; Score 63.5; DB 2; Length 487;  
 Best Local Similarity 30.2%; Pred. No. 7.1;  
 Matches 13; Conservative 12; Mismatches 11; Indels 7; Gaps 1;

RESULT 10  
 I38055

myosin heavy chain, perinatal skeletal muscle - human  
 N:Contains: myosin ATPase (EC 3.6.4.1)

C:Species: Homo sapiens (man)

C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 19-Apr-2002

C:Accession: I38055; JH0154; S12459; S09332; A30220; S49478

R:Julian, E.H.; Kelly, A.M.; Pompidou, A.J.; Hoffman, R.; Schiaffino, S.; Steadman, H

Eur. J. Biochem. 230, 1001-1006, 1995

A:Title: Characterization of a human perinatal myosin heavy-chain transcript.

A:Reference number: I38055; MOID:95324556; PMID:7601129

A:Accession: I38055

A:Status: preliminary; translated from GB/EMBL/DBSJ

A:Molecule type: mRNA

A:Residues: 1-1937 <RES>

A:Cross-references: EMBL:Z38133; NID:g558668; PIDN:CA86293.1; PID:g558669

R:Rarsch-Mitzschl, I.; Peghail, R.; Shows, T.B.; Leitwand, L.A.

Gene 89, 289-294, 1990

A:Title: Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA

A:Reference number: JH0154; MOID:90323631; PMID:2373371

A:Accession: JH0154

A:Molecule type: mRNA

A:Residues: 1-14, 'A', 16-859 <KAR>

A:Cross-references: GB:Y00821

A:Experimental source: skeletal muscle  
 R:Bober, E.  
 submitted to the EMBL Data Library, January 1989  
 A:Reference number: S12458  
 A:Accession: S12459





C:\Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 13-Feb-1998  
C:\Access\on: A02985

C;Accession: A02985

R; Capony, J. P.; Elzinga, M.  
 1987, T 33 1483 1007

Biophys. J. 33, 148a, 1981

A;Reference number: A02985

A;Accession: A02985

A;Molecule type: protein  
A.Residues: 1-258 <CAP>

A;Residues: 1-258 <CAP>

A;Note: this fragment is from the heavy meromyosin subfragment-2 C.Superfamily.v: myosin heavy chain: myosin motor domain homolog

**C: Keywords:** actin binding; ATP-coiled coil; muscle; skeletal myofibril; myosin heavy chain; myosin motor domain homology; superfamily.

C; keywords: actin binding; ATP; coiled coil; muscle; skeletal muscle

Query Match	23.7%;	Score 60;	DB 2;	Length 258;
-------------	--------	-----------	-------	-------------

Best Local Similarity 42.48; Pred. No. 9.6;  
Matches 14; Concentration 8; Winches

Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

QY 21 KEDNVLVESHEKSLG--EANKADVNLTAKASQ 51

153 KEKKAIOEYHOOTI DPIOEEDYHMI MWAKTEP 104

## RESULT 15

S24348

myosin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken (fragment)

C;Species: Gallus gallus (chicken)

```
C:\Date: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
```

C; Accession: S24348

R; Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.

J. MOL. BIOL. 225, 1143-1151, 1992

A; Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform

A;Reference number: S24348; MUID:92309413; PMID:1377278

A;Accession: S24348

A;status: nucleic acid sequence not shown

A; molecule type: mRNA

A;Residues: 1-955 <MOO>

A;Cross-references: EMBL:M74085

C; Superfamily: myosin heavy chain; myosin motor domain homology

C;Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament

Query Match	23.78; Score 60; DB 2; Length 955;
-------------	------------------------------------

Best Local Similarity 42.48; Pred. NO. 38;

Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

21 KEDNVLVESHEKSLG--EANKADVNLTKAKSQ 51

13 КЕККАТООГАУНООМТ ДООГА ХЭРЭВЭЛЭМТЭГЭЭНХЭ 45

Search completed: March 13, 2003, 15:02:26  
Job time : 10.8955 secs

Job time : 10.8955 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2003, 14:52:59 ; Search time 5.70896 Seconds  
(Without alignments)  
370.522 Million cell updates/sec

Title: US-09-636-530-3  
Perfect score: 253  
Sequence: 1 FVALGAPLAPRDAGSQRPK.....KSLGEANKADVNLTKAKSQ 51

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	248	98.0	115	1 PTHY_HUMAN	P01270 homo sapien
2	241	95.3	115	1 PTH_MACFA	Q9X135 macaca fasc
3	206	81.4	115	1 PTHY_CANFA	P52212 canis fami
4	199	78.7	115	1 PTHY_BOVIN	P01268 bos taurus
5	194	76.7	115	1 PTHY_PIG	P01269 sus scrofa
6	160	63.2	115	1 PTHY_PIG	P04089 ratius norv
7	68.5	27.1	119	1 PTHY_CHICK	P15743 gallus gall
8	63	24.9	1937	1 MYH8_HUMAN	P13535 homo sapien
9	61.5	24.3	366	1 YE05_HAEIN	P4180 haemophilus
10	60.5	23.9	555	1 UL25_HSV62	P52537 human herpe
11	60	23.7	1084	1 MYSS_RABIT	P02562 oryctolagus
12	60	23.7	1935	1 MYSS_CYPCA	Q90339 cyprinus ca
13	60	23.7	1938	1 MYH4_RABIT	Q28641 oryctolagus
14	60	23.7	1940	1 MYH3_CHICK	P02565 gallus gall
15	58.5	23.1	527	1 ATRX_RAT	P70486 ratius norv
16	58	22.9	465	1 MYH6_RABIT	P04460 oryctolagus
17	58	22.9	599	1 KLC2_MOUSE	O88448 mus musculu
18	58	22.9	1935	1 MYH7_HUMAN	P12883 homo sapien
19	58	22.9	1935	1 MYH7_PIG	P19293 sus scrofa
20	58	22.9	1935	1 MYH7_RAT	P02564 ratius norv
21	58	22.9	1939	1 MYH1_HUMAN	P12882 homo sapien
22	58	22.9	1941	1 MYH2_HSV6C	Q9UXK2 homo sapien
23	57.5	22.7	555	1 UL25_HSV6C	P52536 human herpe
24	57.5	22.7	378	1 UL25_HSV6C	P52387 human herpe
25	57	22.5	1939	1 MYH4_HUMAN	Q9Y623 homo sapien
26	56	22.1	1938	1 MYSS_CHICK	P13538 gallus gall
27	55.5	21.9	2426	1 SON_HUMAN	P18583 homo sapien
28	55	21.7	831	1 NEFH_RAT	P16884 ratius norv
29	55	21.7	1154	1 KDCG_MESAU	Q64399 mesocricetu
30	55	21.7	1157	1 TE36_CAEEL	P30747 caenorhabdi
31	55	21.7	1518	1 KRK1_YEAST	P42444 saccharomyc
32	55	21.7	1934	1 MYH7_MESAU	P13540 mesocricetu
33	55	21.7	1938	1 MYH6_MOUSE	Q02566 mus musculu

34	55	21.7	1938	1 MYH6_RAT	P02563 ratius norv
35	55	21.7	1939	1 MYH6_MESAU	P13539 mesocricetu
36	54.5	21.5	587	1 GCDA_ACFRE	Q06700 actidinnoco
37	54	21.3	67	1 HARB_PYRAB	Q9Y1F5 pyrococcus
38	54	21.3	67	1 HARB_PYRHO	O74092 pyrococcus
39	54	21.3	325	1 TDG_SCHPO	O59825 schizosacch
40	54	21.3	622	1 KLC2_HUMAN	O9H0B6 homo sapien
41	54	21.3	736	1 MYH7_RABIT	P04461 oryctolagus
42	54	21.3	960	1 VP41_LYCES	P93231 lycopersico
43	54	21.3	983	1 PRPN_RAT	Q63259 ratius norv
44	54	21.3	1033	1 Y328_MYCPN	P75310 mycoplasma
45	53.5	21.1	626	1 CE1B_ECOLI	P04479 escherichia

## ALIGNMENTS

RESULT 1	PTHY_HUMAN	STANDARD:	PRT:	115 AA.
ID	PTHY_HUMAN			
AC	P01270:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).			
GN	PTH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82150870; PubMed=6950381;			
RA	Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;			
RT	"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83169834; PubMed=6220408;			
RA	Vasicek T.J., McDevitt B.E., Freeman M.W., Fennick B.J.,			
RA	Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;			
RT	"Nucleotide sequence of the human parathyroid hormone gene.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).			
RN	[3]			
RP	SEQUENCE OF 26-37.			
RX	MEDLINE=74174967; PubMed=4833516;			
RA	Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;			
RT	"Structural analysis of human parathyroid hormone by a new			
RT	microsequencing approach.";			
RT	Nature 249:155-157(1974).			
RN	[4]			
RP	SEQUENCE OF 32-68.			
RX	MEDLINE=74111656; PubMed=4521809;			
RA	Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,			
RA	O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;			
RT	"The amino-acid sequence of the amino-terminal 37 residues of human			
RT	parathyroid hormone.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).			
RN	[5]			
RP	SEQUENCE OF 61-83 AND 84-115.			
RX	MEDLINE=79082855; PubMed=728431;			
RA	Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,			
RA	Potts J.T. Jr.;			
RT	"Complete amino acid sequence of human parathyroid hormone.";			
RT	Biochemistry 17:5723-5729(1978).			
RN	[6]			
RP	SEQUENCE OF 75-100.			
RA	Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,			
RA	O'Riordan J.L.H., Potts J.T. Jr.;			
RA	(in) Talmadge R.V., Owen M., Parsons J.A. (eds.):			
RL	Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,			
RL	Amsterdam (1975).			

RN [17]  
 RP REVIEWS.  
 RX MEDLINE=75146516; PubMed=1125201;  
 RA Keutman H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;  
 RT "A reinvestigation of the amino-terminal sequence of human  
 RT parathyroid hormone.";  
 RL Biochemistry 14:1842-1847(1975).  
 RN [8]  
 RP SYNTHESIS OF 32-65.  
 RX MEDLINE=75059220; PubMed=4474131;  
 RA Tregear G.W., van Rietschoten J., Green E., Niall H.D.,  
 RA Keutman H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;  
 RT "Solid-phase synthesis of the biologically active N-terminal 1-34  
 RT peptide of human parathyroid hormone.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).  
 RN [9]  
 RP SYNTHESIS OF 32-65.  
 RX MEDLINE=73227467; PubMed=4721748;  
 RA Andreata R.H., Hartmann A., Joehl A., Kamber B., Maier R.,  
 RA Riniker B., Rittel W., Sieder P.;  
 RT "Synthesis of sequence 1-34 of human parathyroid hormone.";  
 RL Helv. Chim. Acta 56:470-473(1973).  
 RN [10]  
 RP STRUCTURE BY NMR OF 32-65.  
 RX MEDLINE=91299748; PubMed=2069952;  
 RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wengender E., Mayer H.;  
 RT "Investigation of the solution structure of the human parathyroid  
 RT hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry,  
 RT and molecular dynamics calculations.";  
 RL Biochemistry 30:6936-6942(1991).  
 RN [11]  
 RP STRUCTURE BY NMR OF 32-65.  
 RX MEDLINE=93345518; PubMed=8344299;  
 RA Barden J.A., Cuthbertson R.M.;  
 RT "Stabilized NMR structure of human parathyroid hormone(1-34).";  
 RL Eur. J. Biochem. 215:315-321(1993).  
 RN [12]  
 RP STRUCTURE BY NMR OF 32-68.  
 RX MEDLINE=95318084; PubMed=7797503;  
 RA Marx U.C., Austermann S., Bayer P., Adermann K., Eychart A.,  
 RA Sticht H., Walter S., Schmid F.-X., Jeneicke R., Forssmann W.-G.,  
 RA Roesch P.;  
 RT "Structure of human parathyroid hormone 1-37 in solution.";  
 RL J. Biol. Chem. 270:15194-15202(1995).  
 RN [13]  
 RP STRUCTURE BY NMR OF 32-70.  
 RX MEDLINE=20090619; PubMed=10623601;  
 RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;  
 RT "Solution structures of human parathyroid hormone fragments  
 RT hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment  
 RT bPTH(1-37).";  
 RL Biochem. Biophys. Res. Commun. 267:213-220(2000).  
 RN [14]  
 RP VARIANT ARG-18.  
 RX MEDLINE=91009811; PubMed=2212001;  
 RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,  
 RA Kroenberg H.M.;  
 RT "Mutation of the signal peptide-encoding region of the  
 RT preproparathyroid hormone gene in familial isolated  
 RT hypoparathyroidism.";  
 RL J. Clin. Invest. 86:1084-1087(1990).  
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED  
 CC HYPOPARATHYROIDISM (FTH).  
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
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 CC -----  
 DR EMBL: J00301; AAA60215.1; -  
 DR EMBL: V00597; CAA23843.1; -  
 DR EMBL: A29146; CAA01956.1; -  
 DR PIR: A01536; PTHU  
 DR PIR: A19339; A19339.  
 DR PDB: 1HPH; 10-JUL-95.  
 DR PDB: 1HTH; 15-OCT-97.  
 DR PDB: 1ZWA; 12-MAR-97.  
 DR PDB: 1ZWB; 12-MAR-97.  
 DR PDB: 1ZWD; 12-MAR-97.  
 DR PDB: 1ZWE; 12-MAR-97.  
 DR PDB: 1ZWF; 16-JUN-97.  
 DR PDB: 1ZWG; 16-JUN-97.  
 DR PDB: 1BWK; 14-JAN-00.  
 DR PDB: 1HPY; 14-JAN-00.  
 DR Genew; HGNC:9606; PTH.  
 DR MIM: 146200; -.  
 DR MIM: 168450; -.  
 DR InterPro: IPR001415; Parathyrd\_hrm.  
 DR InterPro: IPR003625; Pthyrdorm\_sub.  
 DR Pfam: PF01279; Parathyroid; 1.  
 DR ProDom: PD010687; Pthyrdorm\_sub; 1.  
 DR SMART: SM00087; PTH; 1.  
 DR PROSITE: PS00335; PARATHYROID; 1.  
 KW Hormone; Signal; Disease mutation; 3D-structure.  
 FT SIGNAL 1 25  
 FT PROPEP 26 31  
 FT CHAIN 32 115  
 FT VARIANT 18 18  
 FT -----  
 FT PARATHYROID HORMONE.  
 FT C-> R (IN FTH, LEADS TO INEFFICIENT  
 FT PROCESSING OF THE PRECURSOR).  
 FT /FTID=VAR\_006047.  
 FT N-> D (IN REF. 5).  
 SQ SEQUENCE 115 AA; 12861 MW; 849015736A6E5597 CRC64;  
 QY 1 FVALGAPLAPRAGSGPRKKEDNVLYESHESIGKANKADVNLTKAKSQ 51  
 DB 65 FVALGAPLAPRAGSGPRKKEDNVLYESHESIGKANKADVNLTKAKSQ 115  
 RESULT 2  
 ID PTH\_MACFA STANDARD; PRT; 115 AA.  
 AC Q9XT35;  
 DT 16-OCT-2001 (Rel. 40; Created)  
 DT 16-OCT-2001 (Rel. 40; Last sequence update)  
 DT 16-OCT-2001 (Rel. 40; Last annotation update)  
 DE Parathyroid hormone precursor (Parathyrin) (PTH).  
 GN PTH.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Malaviljitmond S., Takenaka O.;  
 RT "Nucleotide sequences of parathyroid gene in five species of macaque  
 RT of Thailand.";  
 RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).  
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
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 CC -----  
 DR EMBL: AF130257; AADA2777.1; -.  
 DR HSP: P01270; IHP.  
 DR InterPro: IPR001415; Parathyrd\_hrm.  
 DR InterPro: IPR003625; Pthyrdorm\_sub.  
 DR Pfam: PF01279; Parathyroid.1.  
 DR ProDom: PD010687; Pthyrdorm\_sub.1.  
 DR SMART: SM00087; PTH.1.  
 DR PROSITE: PS00335; PARATHYROID.1.  
 KW Hormone; Signal.  
 FT SIGNAL 1 25 BY SIMILARITY.  
 FT PROPEP 26 31 BY SIMILARITY.  
 FT CHAIN 32 115 PARATHYROID HORMONE.  
 SQ SEQUENCE 115 AA: 12890 MW: 8C2500DF24B5E597 CRC64;  
 Query Match 95.3%; Score 241; DB 1; Length 115;  
 Best Local Similarity 92.2%; Pred. No. 8.4e-23;  
 Matches 47; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADYVNLTKAKSQ 51  
 DB 65 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEADKADYVNLTKAKSQ 115  
 RESULT 3  
 ID PTHX\_CANFA STANDARD: PRT: 115 AA.  
 AC P52212;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Parathyroid hormone precursor (Parathyrin) (PTH).  
 GN PTH.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Parathyroid;  
 RX MEDLINE=95369696; PubMed=7642102;  
 RA Rosol T.J., Steinmeyer C.L., McCauley L.K., Greene A.,  
 RA Deville J.W., Capen C.C.;  
 RT "Sequences of the cDNAs encoding canine parathyroid hormone-related  
 RT protein and parathyroid hormone.";  
 RT Gene 160:241-243(1995).  
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
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 CC -----  
 DR EMBL: U15662; AAA82584.1; -.  
 DR HSP: P01268; 1ZNC.  
 DR InterPro: IPR001415; Parathyrd\_hrm.  
 DR InterPro: IPR003625; Pthyrdorm\_sub.  
 DR Pfam: PF01279; Parathyroid.1.  
 DR ProDom: PD010687; Pthyrdorm\_sub.1.  
 DR SMART: SM00087; PTH.1.  
 DR PROSITE: PS00335; PARATHYROID.1.  
 KW Hormone; Signal.  
 FT SIGNAL 1 25 BY SIMILARITY.  
 FT PROPEP 26 31 BY SIMILARITY.  
 FT CHAIN 32 115 PARATHYROID HORMONE.

SQ SEQUENCE 115 AA: 12957 MW: FC38F77F1C8CE56 CRC64;  
 Query Match 81.4%; Score 206; DB 1; Length 115;  
 Best Local Similarity 82.4%; Pred. No. 1.6e-18;  
 Matches 42; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEANKADYVNLTKAKSQ 51  
 DB 65 FVALGAPLAPRDAGSORPRKKEDNVLVESHEKSLGEADKADYVNLTKAKSQ 115  
 RESULT 4  
 ID PTHX\_BOVIN  
 ID PTHX\_BOVIN STANDARD: PRT: 115 AA.  
 AC P01268;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Parathyroid hormone precursor (Parathyrin) (PTH).  
 GN PTH.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80056617; PubMed=388425;  
 RA Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,  
 RA Potts J.T. Jr., Rich A.;  
 RT "Cloning and nucleotide sequence of DNA coding for bovine  
 RT preproparathyroid hormone.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82037785; PubMed=6170060;  
 RA Weaver C.A., Gordon D.F., Kemper B.;  
 RT "Introduction by molecular cloning of artifactual inverted sequences  
 RT at the 5' terminus of the sense strand of bovine parathyroid hormone  
 RT cDNA.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83105964; PubMed=6185374;  
 RA Weaver C.A., Gordon D.F., Kemper B.;  
 RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";  
 RT Mol. Cell. Endocrinol. 28:411-424(1982).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84262483; PubMed=6086460;  
 RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;  
 RT "Isolation and complete nucleotide sequence of the gene for bovine  
 RT parathyroid hormone.";  
 RT Gene 28:319-329(1984).  
 RN [5]  
 RP SEQUENCE OF 26-115.  
 RX MEDLINE=74142666; PubMed=4522780;  
 RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,  
 RA Cohn D.V.;  
 RT "The N-terminal amino-acid sequence of bovine preproparathyroid  
 RT hormone.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).  
 RN [6]  
 RP SEQUENCE OF 32-115.  
 RX MEDLINE=71076162; PubMed=5531031;  
 RA Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,  
 RA Aubach G.D., Potts J.T. Jr.;  
 RT "The amino acid sequence of bovine parathyroid hormone I.";  
 RT Hope-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).  
 RN [7]  
 RP SEQUENCE OF 32-115.  
 RX MEDLINE=71063634; PubMed=5275384;  
 RA Brewer H.B. Jr., Roman R.;

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RT "Bovine parathyroid hormone: amino acid sequence."
RL Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE=71091588; PubMed=4322265;
RA Potts J.T., Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RT Defeo L.J., Dawson B.F., Hogan M.L., Aurbach G.D.,
RT "Synthesis of a biologically active N-terminal tetratriacontapeptide
RL of parathyroid hormone."
RL Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN [9]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE=20090619; PubMed=10623601;
RA Marx U.C., Adelman K., Bayer P., Forssmann W.-G., Rosch P.;
RT "Solution structures of human parathyroid hormone fragments
RT hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
RT hPTH(1-37)."
RL Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL: V00106; CAA3439.1; -
DR EMBL: J00024; AAA30747.1; -
DR EMBL: K01938; AAA30749.1; -
DR EMBL: M25082; AAA30748.1; -
DR PIR: A01534; PTBO.
DR PIR: A24949; A24949.
DR PDB: 1ZWC; 12-MAR-97.
DR InterPro: IPR001415; Parathyrd_hrm.
DR InterPro: IPR003625; Pthyrdorm_sub.
DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthyrdorm_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.
KW Hormone; Signal; 3D-structure.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4)
SQ SEQUENCE 115 AA; 12980 MW; 2ED246B348880710 CRC64;

Query Match 78.7%; Score 199; DB 1; Length 115;
Best Local Similarity 80.4%; Pred. No. 1.2e-17;
Matches 41; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKEDNVLVESHEKSLGANKADVVLTKAKSQ 51
DB 65 FVALGASIVHRDGGSORPRKEDNVLVESHQKSLGADRAADVVLTKAPQ 115

RESULT 5
PTHY_PIG STANDARD; PRT; 115 AA.
AC P01269;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN PTH.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
RT preproparathyroid hormone from pig and rat."
RL Nucleic Acids Res. 15:6740-6740(1987).
RN [2]
RP SEQUENCE OF 26-115.
RX MEDLINE=76018954; PubMed=1164500;
RA Chu L.L.H., Huang W.-Y., Littlelike E.T., Hamilton J.W., Cohn D.V.;
RT "Porcine preproparathyroid hormone. Identification, biosynthesis, and
RT partial amino acid sequence."
RL Biochemistry 14:3631-3635(1975).
RN [3]
RP SEQUENCE OF 32-115.
RX MEDLINE=74253317; PubMed=4840833;
RA Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RT Potts J.T., Jr.;
RL Biochemistry 13:1994-1999(1974).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL: X05722; CAA29193.1; -
DR PIR: A01535; PTPG.
DR PIR: B26806; B26806.
DR HSSP: P01270; 1BWY.
DR InterPro: IPR001415; Parathyrd_hrm.
DR InterPro: IPR003625; Pthyrdorm_sub.
DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthyrdorm_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
SQ SEQUENCE 115 AA; 12852 MW; 9FE8BCDE614BAC16 CRC64;

Query Match 76.7%; Score 194; DB 1; Length 115;
Best Local Similarity 78.4%; Pred. No. 4.9e-17;
Matches 40; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKEDNVLVESHEKSLGANKADVVLTKAKSQ 51
DB 65 FVALGASIVHRDGGSORPRKEDNVLVESHQKSLGADRAADVVLTKAPQ 115

RESULT 6
PTHY_RAT STANDARD; PRT; 115 AA.
AC P04089; Q63473;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN PTH.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84135846; PubMed=6321505;
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RA Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.,  
 RT "Gene encoding parathyroid hormone. Nucleotide sequence of the rat  
 RT gene and deduced amino acid sequence of rat preproparathyroid  
 RT hormone.";  
 RL J. Biol. Chem. 259:3320-3329(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87316938; PubMed=3628009;  
 RA Schmeller H.-J., Gross G., Widera G., Mayer H.;  
 RT "Nucleotide sequence of a full-length cDNA clone encoding  
 RT preproparathyroid hormone from pig and rat.";  
 RL Nucleic Acids Res. 15:6740-6740(1987).  
 RN [3]  
 RP SEQUENCE OF 10-115 FROM N.A.  
 RC TISSUE=Parathyroid;  
 RA Schmeller H.-J., Gross G., Mayer H.;  
 RT "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid  
 RT hormone.";  
 RL Adv. Gene Technol. 21:228-229(1984).  
 RN [4]  
 RP SEQUENCE OF 32-115 FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain, Parathyroid, and Liver;  
 RX MEDLINE=96079910; PubMed=758314;  
 RA Nutley M.T., Parimi S.A., Harvey S.;  
 RT "Sequence analysis of hypothalamic parathyroid hormone messenger  
 RT ribonucleic acid.";  
 RL Endocrinology 136:5600-5607(1995).  
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
 CC -1- TISSUE SPECIFICITY: HYPOTHALAMUS AND PARATHYROID GLAND.  
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
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 CC -----  
 CC  
 DR EMBL, K01268; AAA1979.1; -;  
 DR EMBL, X05721; CAA29192.1; -;  
 DR EMBL, M54875; AAA57156.1; -;  
 DR EMBL, S80127; -; NOT\_ANNOTATED\_CDS.  
 DR PIR, A05091; A05091.  
 DR PIR, A26806; A26806.  
 DR HSSP, P01270; 1ZWB.  
 DR InterPro: IPR001415; Parathyrd\_hrm.  
 DR InterPro: IPR003625; Pthythorm\_sub.  
 DR Pfam: PF01279; Parathyroid.1.  
 DR ProDom: PD010687; Pthythorm\_sub.1.  
 DR SMART; SM00087; PTH; 1.  
 DR PROSITE; PS00335; PARATHYROID; 1.  
 DR Hormone; Signal.  
 FT SIGNAL 1 25  
 FT PROPEP 26 31  
 FT CHAIN 32 115 PARATHYROID HORMONE.  
 FT CONFLICT 18 18 C -> Y (IN REF. 3).  
 FT CONFLICT 23 23 A -> T (IN REF. 3).  
 FT CONFLICT 33 33 V -> I (IN REF. 3).  
 FT CONFLICT 62 62 V -> G (IN REF. 3).  
 SQ SEQUENCE 115 AA; 12722 MW; 7BA34CFCAS28B230 CRC64;

Query Match 63.2%; Score 160; DB 1; Length 115;  
 Best Local Similarity 62.7%; Pred. No. 7.2e-13;  
 Matches 32; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

OY 1 EVALAPLAPRDAGSORPRKEDNVLVESHKSLGSEANKADVNLTKAKSO 51  
 DB 65 FVSLGVQMAARSGSYORPTKKEENVLVDSNKSLSGDKADVDVLYAKAKSO 115

RESULT 7

PTHY\_CHICK  
 ID PTHY\_CHICK STANDARD; PRT; 119 AA.  
 AC P15743;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Parathyroid hormone precursor (PTH).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89219100; PubMed=2710135;  
 RA Russell J., Sherwood L.M.;  
 RT "Nucleotide sequence of the DNA complementary to avian (chicken)  
 RT preproparathyroid hormone mRNA and the deduced sequence of the  
 RT hormone precursor.";  
 RL Mol. Endocrinol. 3:325-331(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89284968; PubMed=3251402;  
 RA Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,  
 RA Kronenberg H.M.;  
 RT "Nucleotide sequence of cloned cDNAs encoding chicken  
 RT preproparathyroid hormone.";  
 RL J. Bone Miner. Res. 3:689-698(1988).  
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
 CC -----  
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 CC -----  
 CC  
 DR EMBL, M31604; AAA49093.1; -;  
 DR EMBL, M36522; AAB02866.1; -;  
 DR PIR, A34937; A34937.  
 DR HSSP, P01270; 1HPY.  
 DR InterPro: IPR001415; Parathyrd\_hrm.  
 DR InterPro: IPR003625; Pthythorm\_sub.  
 DR Pfam: PF01279; Parathyroid.1.  
 DR ProDom: PD010687; Pthythorm\_sub.1.  
 DR SMART; SM00087; PTH; 1.  
 DR PROSITE; PS00335; PARATHYROID; 1.  
 DR Hormone; Signal.  
 FT SIGNAL 1 25  
 FT PROPEP 26 31  
 FT CHAIN 32 119 PARATHYROID HORMONE.  
 FT CONFLICT 32 119  
 SQ SEQUENCE 119 AA; 13943 MW; B309D8E772997F6E CRC64;

Query Match 27.1%; Score 68.5; DB 1; Length 119;  
 Best Local Similarity 38.9%; Pred. No. 0.12;  
 Matches 21; Conservative 6; Mismatches 14; Indels 13; Gaps 1;

OY 9 APRDAGSORPRKEDNVLVESHKSLGSEANKADVNLTKAK 49  
 DB 65 ALEDARTQRPKNKEDVIVLGEIRNRRLPEHLRAAYQKKSIDDKAYMNVLFKK 118

RESULT 8  
 MYH8\_HUMAN STANDARD; PRT; 1937 AA.  
 ID MYH8\_HUMAN  
 AC P13535; Q14910;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Myosin heavy chain, skeletal muscle, perinatal (MyHC-perinatal).

GN MYH8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=90323631; PubMed=2373371;  
 RA Karsch-Mizrachi I., Peghali R., Shows T.B. Jr., Leinwand L.A.;  
 RT "Generation of a full-length human perinatal myosin heavy-chain-  
 RL encoding cDNA.";  
 RL Gene 89:289-294(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=95324556; PubMed=7601129;  
 RA Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S.,  
 RT Characterization of a human perinatal myosin heavy-chain  
 transcript.";  
 RL Eur. J. Biochem. 230:1001-1006(1995).  
 RN [3]  
 RP SEQUENCE OF 502-1937 FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=90335862; PubMed=1691980;  
 RA Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,  
 RT Arnold H.H.;  
 RT "Identification of three developmentally controlled isoforms of human  
 RT myosin heavy chains.";  
 RL Eur. J. Biochem. 189:55-65(1990).  
 RN [4]  
 RP SEQUENCE OF 860-1937 FROM N.A.  
 RX MEDLINE=89234168; PubMed=2715179;  
 RA Peghali R., Leinwand L.A.;  
 RT "Molecular genetic characterization of a developmentally regulated  
 RT human perinatal myosin heavy chain.";  
 RL J. Cell Biol. 108:1791-1797(1989).  
 RN [5]  
 RP SEQUENCE OF 1-46 FROM N.A.  
 RA Esser K., Tidhar A., Myszkowski M.;  
 RT "Isolation and characterization of the human perinatal MHC promoter.";  
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: MUSCLE CONTRACTION.  
 CC -1- SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING  
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,  
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY  
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.  
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE  
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED  
 CC SUBFRAGMENT (S2).  
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: M36769; AAC17185.1; -;  
 DR EMBL: Z38133; CAA86293.1; -;  
 DR EMBL: X51592; CAA35941.1; -;  
 DR EMBL: AF067143; AAC21557.1; -;  
 DR PIR: A30220; A30220.

DR HSSP; P13538; 2MYS.  
 DR Genew; HGNC:7578; MYH8.  
 DR MIM; 160741; -;  
 DR InterPro; IPR000048; IQ\_region.  
 DR InterPro; IPR004003; Myosin\_N.  
 DR InterPro; IPR002928; Myosin\_Tail.  
 DR InterPro; IPR001609; myosin\_head.  
 DR Pfam; PF00663; myosin\_head.  
 DR Pfam; PF00612; IQ; 1.  
 DR Pfam; PF01576; Myosin\_tail; 1.  
 DR Pfam; PF02736; Myosin\_N; 1.  
 DR PRINTS; PR00193; MYOSINHEAVY.  
 DR PRODOM; PD000355; myosin\_head; 1.  
 DR SMART; SM00015; IQ; 1.  
 DR SMART; SM00242; MYSC; 1.  
 DR PROSITE; PS50096; IQ; 1.  
 KW Myosin; muscle protein; coiled coil; thick filament; Actin-binding;  
 KW ATP-binding; Methylation; Alkylation; Multigene family;  
 KW Calmodulin-binding.  
 FT DOMAIN 1 780  
 FT MYOSIN HEAD-LIKE.  
 FT DOMAIN 813  
 FT COILED COIL (POTENTIAL).  
 FT NP\_BIND 181 188  
 FT ATP.  
 FT DOMAIN 658 680  
 FT ACTIN-BINDING.  
 FT MOD\_RES 760 774  
 FT METHYLATION (TRI-) (POTENTIAL).  
 FT MOD\_RES 132 132  
 FT ALKYLATION (SH-1) (POTENTIAL).  
 FT MOD\_RES 698 698  
 FT ALKYLATION (SH-2) (POTENTIAL).  
 FT MOD\_RES 708 708  
 FT A -> R (IN REF. 2).  
 FT CONFLICT 15 15  
 FT E -> Q (IN REF. 1 AND 4).  
 FT CONFLICT 970 970  
 FT M -> N (IN REF. 3).  
 FT CONFLICT 1072 1072  
 FT N -> H (IN REF. 1 AND 4).  
 FT CONFLICT 1247 1247  
 FT MC -> DGG (IN REF. 3).  
 FT CONFLICT 1251 1252  
 FT E -> G (IN REF. 1 AND 4).  
 FT CONFLICT 1261 1261  
 FT K -> Q (IN REF. 1 AND 4).  
 FT CONFLICT 1297 1297  
 FT KY -> NT (IN REF. 3).  
 FT CONFLICT 1377 1378  
 FT EN -> AH (IN REF. 1 AND 4).  
 FT CONFLICT 1504 1505  
 FT E -> D (IN REF. 1 AND 4).  
 FT CONFLICT 1847 1847  
 FT D -> H (IN REF. 2).  
 FT CONFLICT 1914 1914  
 SQ SEQUENCE 1937 AA; 222762 MW; A3BE2D151792E9E8 CXC64;  
 Query Match 24.98; Score 63; DB 1; Length 1937;  
 Best Local Similarity 42.48; Pred. No. 14;  
 Matches 14; Conservativity 9; Mismatches 8; Indels 2; Gaps 1;  
 QY 21 KEDNVVESHKSG--EANKADNVLTAKSQ 51  
 DB 997 KKKALQETHQOQTLDDQLQAEEDKVNILTKAKTK 1029  
 RESULT 9  
 YE05\_HAEIN STANDARD; PRT; 366 AA.  
 AC P4180;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein H11405.  
 GN H11405.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 CC Haemophilus.  
 CX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Rd / KW20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Uutterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,



RA Fine L.D., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
 RT Rd.";  
 RL Science 269:496-512(1995).  
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 CC -----  
 CC EMBL: U32820; AAC23055.1; -;  
 DR TIGR: H11405; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 366 AA; 40122 MW; 6804080B631AEC0 CRC64;  
 Query Match 24.3%; Score 61.5; DB 1; Length 366;  
 Best Local Similarity 35.6%; Pred. No. 3.2;  
 Matches 16; Conservative 10; Mismatches 18; Indels 1; Gaps 1;  
 Oy 7 PLAPDAGSQRPKKEDNVLVESHKSLGEANKADVNLTKASQ 51  
 Db 222 PKPKKKSEPKKKEDVKEKLEKSL-KAKDERIQLKDAQAK 265  
 ID UL25\_HSV62 STANDARD; PRT; 555 AA.  
 AC P52537;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Vitron protein U50.  
 GN U50 OR KALLR.  
 OS Human herpesvirus (type 6 / strain 229) (HHV6)  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Roseolovirus.  
 OX NCBI\_TaxID=36351;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95074921; PubMed=7983761;  
 RA Stamey F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.;  
 RT "Intergenic linear amplification of human herpesvirus 6b orilyt  
 RT J. Virol. 69:589-596(1995)."  
 CC -----  
 CC -1- FUNCTION: VIRION PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,  
 CC EHV-1 36, EBV BFRF1, HCMV UL77, ILTV ORF2, AND VZV 34.  
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 CC -----  
 CC EMBL: AF157706; AAB06348.1; -;  
 DR InterPro: IPR002493; UL25.  
 DR Pfam: PF01499; UL25.1.  
 SO SEQUENCE 355 AA; 63830 MW; 68B86590DC4CD2BC CRC64;  
 Query Match 23.9%; Score 60.5; DB 1; Length 555;  
 Best Local Similarity 42.5%; Pred. No. 6.8;  
 Matches 17; Conservative 8; Mismatches 10; Indels 5; Gaps 2;  
 Oy 16 ORPKKEDNVLVESHKSLGEA-----NKADVNLTKASQ 51  
 Db 67 ORKQKSDVLT-NSHLKAIEDALFTNDGEVNVETKADQ 105

RESULT 11  
 MYSS\_RABIT  
 ID MYSS\_RABIT STANDARD; PRT; 1084 AA.  
 AC P02562;  
 DT 21-JUL-1966 (Rel. 01, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUL-1996 (Rel. 36, Last annotation update)  
 DE Myosin heavy chain, skeletal muscle (Fragments).  
 OS Oryctolagus cuniculus (Rabbit).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 CC NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE OF 1-258.  
 RA Capony J.-P., Elzinga M.;  
 RT "The amino acid sequence of A 34,000 dalton fragment from S-2 of  
 RT myosin.";  
 RL Biophys. J. 33:148A-148A(1981).  
 RN [2]  
 RP SEQUENCE OF 259-428.  
 RX MEDLINE=85131142; PubMed=3972832;  
 RA Lu R.C., Wong A.;  
 RT "The amino acid sequence and stability predictions of the hinge  
 RT region in myosin subfragment 2.";  
 RL J. Biol. Chem. 260:3456-3461(1985).  
 RN [3]  
 RP SEQUENCE OF 409-1084 FROM N.A.  
 RX MEDLINE=87304245; PubMed=3305014;  
 RA Maeda K., Szekiel G., Wittinghofer A.;  
 RT "Characterization of cDNA coding for the complete light meromyosin  
 RT portion of a rabbit fast skeletal muscle myosin heavy chain.";  
 RL Eur. J. Biochem. 167:97-102(1987).  
 CC -----  
 CC -1- FUNCTION: MUSCLE CONTRACTION.  
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
 CC -----  
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING  
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,  
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE  
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED  
 CC SUBFRAGMENT (S2).  
 CC -1- SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES,  
 CC WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE  
 CC CONSERVED.  
 CC -----  
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 CC -----  
 CC EMBL: X05958; CAA29391.1; -;  
 DR PIR: A02985; A02985.  
 DR PIR: A05280; A05280.  
 DR PIR: S00084; S00084.  
 KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;  
 KW ATP-binding; Multigene family.  
 FT NON\_TER 1  
 FT DOMAIN <1>258 ALPHA-HELICAL TAILPIECE (S2).  
 FT NON\_CONS 258 259 RODLIKE TAIL (S2 AND LHM DOMAINS).  
 FT DOMAIN <259 1084 COILED COIL (POTENTIAL).  
 FT VARIANT 455 1084 L -> V.  
 FT VARIANT 405 405 L -> V.  
 FT VARIANT 408 408 V -> L.  
 FT VARIANT 421 421 E -> D.  
 FT VARIANT 423 423 S -> G.

FT	VARIANT	426	426	K -> R.
SO	SEQUENCE	1084 AA;	125488 MM;	229CFD6A61F7F0 CRC64;
	Query Match	23.7%;	Score 60;	DB 1; Length 1084;
	Best Local Similarity	42.4%;	Pred. NO. 17;	
	Matches 14;	Conservative	8;	Mismatches 9; Indels 2; Gaps 1.
QY	21 KEDNVLVESHEKSLG--EANKADVAVLTFRKQSO 51			
DB	152 KKKKALQEAHQQTLDLDQAEKDVKVTLYTKAKTK 184			
	RESULT 12			
WSS_CYPCA				
ID	WSS_CYPCA	STANDARD;	PRT:	1935 AA.
AC	Q90339;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Myosin heavy chain, fast skeletal muscle.			
OS	Cyprinus carpio (Common carp).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Cyprinus.			
OX	NCBI_TaxID=7962;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fast muscle;			
RC	MEDLINE=97352533; PubMed=9208928;			
RA	Hirayama Y., Watabe S.;			
RT	"Structural differences in the crossbridge head of temperature-associated myosin subfragment-1 isoforms from carp fast skeletal muscle.";			
RT	Eur. J. Biochem. 246:380-387(1997).			
RL	[2]			
RP	SEQUENCE OF 981-1935 FROM N.A.			
RC	TISSUE=Fast muscle;			
RC	MEDLINE=97176447; PubMed=9023993;			
RA	Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;			
RT	"cDNA cloning of myosin heavy chain isoforms from carp fast skeletal muscle and their gene expression associated with temperature acclimation.";			
RT	J. Exp. Biol. 200:27-34(1997).			
RL	[3]			
RN	SEQUENCE OF 1387-1528 FROM N.A.			
RP	MEDLINE=95194396; PubMed=7887920;			
RA	Watabe S., Imai J., Nakaya M., Hirayama Y., Okamoto Y., Masaki H.,			
RA	Uozumi T., Hirose I., Aoki T.;			
RT	"Temperature acclimation induces light meromyosin isoforms with different primary structures in carp fast skeletal muscle.";			
RT	Biochem. Biophys. Res. Commun. 208:118-125(1995).			
RL	-1- FUNCTION: MUSCLE CONTRACTION.			
CC	-1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)			
CC	AND 2 REGULATOR LIGHT CHAIN SUBUNITS (MLC-2).			
CC	-1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.			
CC	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,			
CC	CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.			
CC	-1- PPM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY			
CC	ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.			
CC	-1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT			
CC	MEROMYOSIN (LMN) AND 1 HEAVY MEROMYOSIN (HNM). IT CAN LATER BE			
CC	SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED			
CC	SUBFRAGMENT (S2).			
CC	-1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.			
CC	-----			
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CC -----
DR EMBL, D89992; BAA2069.1; -.
DR EMBL, D50476; BAA09069.1; -.
DR EMBL, D43700; BAA07802.1; -.
DR HSSP: P13538; 2MS.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF00612; IQ; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR Prodom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; 1.
KW Myosin; muscle protein; Coiled coil; Thick filament; Actin-binding;
KW ATP-binding; Methylation; Alkylation; Calmodulin-binding;
KW Multigene family.
FT DOMAIN 1 781 MYOSIN HEAD-LIKE.
FT DOMAIN 782 811 IQ.
FT DOMAIN 812 839 HINGE.
FT DOMAIN 840 1935 COILED COIL (POTENTIAL).
FT NP_BIND 178 185 ATP (POTENTIAL).
FT DOMAIN 659 681 ACTIN-BINDING.
FT DOMAIN 761 775 ACTIN-BINDING.
FT MOD_RES 129 129 METHYLATION (TRI-) (POTENTIAL).
FT MOD_RES 699 699 ALKYLATION (SH-1).
FT MOD_RES 709 709 ALKYLATION (SH-2).
SQ SEQUENCE 1935 AA; 221599 BW; 9A1244B67D63C83B CRC64;

Query Match 23.7%; Score 60; DB 1; Length 1935;
Best Local Similarity 42.4%; Pred. No. 32;
Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

OY 21 KEDNVLSHSKSLG--EANKADVNVLTIRKASQ 51
|| | | | | | | | | | | | | | | | | | | |
Db 995 KKKKALQEHQHTLDDLQAEEDKVTITRKATK 1027

RESULT 13
MYH4_RABIT
ID MYH4_RABIT STANDARD; PRT; 1938 AA.
AC 028641;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Myosin heavy chain, skeletal muscle, juvenile.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Skeletal muscle;
RA Maeda K., Hostinova E., Roesch-Kleinlauf A., Schuster H., Gasperik J.,
RA Wittinghofer A.;
RT "Isolation, sequencing of myosin heavy chain cDNA from rabbit
RT skeletal muscle and a novel cosynthesis of S-1 fragment with the
RT essential and regulatory light chains.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MUSCLE CONTRACTION.
CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC -!- DOMAIN: THE ROD-LIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

```

CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE  
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED  
 CC SUBFRAGMENT (S2).  
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U3574; AAA74199.1; -  
 DR HSP: P1358; 2MS.  
 DR InterPro: IPR000048; IO\_region.  
 DR InterPro: IPR004009; Myosin\_N.  
 DR InterPro: IPR002928; Myosin\_tail.  
 DR InterPro: IPR001609; myosin\_head.  
 DR Pfam: PF00063; myosin\_head; 1.  
 DR Pfam: PF00612; IO; 2.  
 DR Pfam: PF01576; Myosin\_tail; 1.  
 DR Pfam: PF02736; Myosin\_N; 1.  
 DR PRINTS: PR00193; MYOSINHEAVY.  
 DR PRODOM: PD000355; myosin\_head; 1.  
 DR SMART: SM00015; IO; 1.  
 DR SMART: SM00242; MYSC; 1.  
 DR PROSITE: PS50096; IO; 1.  
 KW Myosin: Muscle protein; Coiled coil; Thick filament; Actin-binding;  
 KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;  
 KW Multigene family.  
 FT DOMAIN 1 783 MYOSIN HEAD-LIKE.  
 FT DOMAIN 784 813 IO.  
 FT DOMAIN 842 1938 COILED COIL (POTENTIAL).  
 FT NP\_BIND 179 186 ATP (POTENTIAL).  
 FT DOMAIN 658 680 ACTIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 760 774 ACTIN-BINDING (BY SIMILARITY).  
 FT MOD\_RES 35 35 METHYLATION (MONO-) (BY SIMILARITY).  
 FT MOD\_RES 130 130 METHYLATION (TRI-) (BY SIMILARITY).  
 FT MOD\_RES 552 552 METHYLATION (TRI-) (BY SIMILARITY).  
 FT MOD\_RES 756 756 METHYLATION (TRI-) (BY SIMILARITY).  
 FT MOD\_RES 698 698 ALKYLATION (SH-1) (BY SIMILARITY).  
 FT MOD\_RES 708 708 ALKYLATION (SH-2) (BY SIMILARITY).  
 SQ SEQUENCE 1938 AA; 223064 MW; D8A8A2EC5B182626 CRC64;  
 Query Match 23.7%; Score 60; DB 1; Length 1938;  
 Best Local Similarity 42.4%; Pred. No. 32;  
 Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;  
 Oy 21 KEDNVIVESHESLGS--EANKADVNVLTAKSQ 51  
 Db 997 KKKKALQEAHQCTLDLQAEEDKVNLTAKKTK 1029  
 RESULT 14  
 MYH3\_CHICK STANDARD; PRT; 1940 AA.  
 AC P02565;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Myosin heavy chain, fast skeletal muscle, embryonic.  
 GN MYH3.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87194881; PubMed=3571266;

RA Molina M.I., Kropp K.E., Gulick J., Robbins J.;  
 RT "The sequence of an embryonic myosin heavy chain gene and isolation  
 RT of its corresponding cDNA."  
 RL J. Biol. Chem. 262:6478-6488(1987).  
 RN [2]  
 RP SEQUENCE OF 1502-1940 FROM N.A.  
 RX MEDLINE=83161144; PubMed=6833296;  
 RA Kavanay C.J., Ubeda P.K., Sinha A.M., Elzinga M., Tong S.W., Zak R.,  
 RA Jakovic S., Rabinowitz M.;  
 RT "Cloned mRNA sequences for two types of embryonic myosin heavy chains  
 RT from chick skeletal muscle. I. DNA and derived amino acid sequence of  
 RT light meromyosin."  
 RL J. Biol. Chem. 258:5196-5205(1983).  
 CC -1- FUNCTION: MUSCLE CONTRACTION.  
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
 CC HEAVY CHAIN SUBUNITS (MHC) 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING  
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,  
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY  
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.  
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE  
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED  
 CC SUBFRAGMENT (S2).  
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: V00430; CAA23712.1; -  
 DR EMBL: J02714; AAA48972.1; -  
 DR PIR: A02990; A02990.  
 DR PIR: A29320; A29320.  
 DR HSP: P13538; 2MS.  
 DR InterPro: IPR000048; IO\_region.  
 DR InterPro: IPR004009; Myosin\_N.  
 DR InterPro: IPR002928; Myosin\_tail.  
 DR Pfam: PF00063; myosin\_head; 1.  
 DR Pfam: PF00612; IO; 2.  
 DR Pfam: PF01576; Myosin\_tail; 1.  
 DR Pfam: PF02736; Myosin\_N; 1.  
 DR PRINTS: PR00193; MYOSINHEAVY.  
 DR PRODOM: PD000355; myosin\_head; 1.  
 DR SMART: SM00015; IO; 1.  
 DR SMART: SM00242; MYSC; 1.  
 DR PROSITE: PS50096; IO; 1.  
 KW Myosin: Muscle protein; Coiled coil; Thick filament; Actin-binding;  
 KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;  
 KW Multigene family.  
 FT DOMAIN 1 785 MYOSIN HEAD-LIKE.  
 FT DOMAIN 786 815 IO.  
 FT DOMAIN 844 1940 COILED COIL (POTENTIAL).  
 FT NP\_BIND 179 186 ATP.  
 FT DOMAIN 660 682 ACTIN-BINDING.  
 FT DOMAIN 762 776 ACTIN-BINDING.  
 FT MOD\_RES 130 130 METHYLATION (TRI-) (POTENTIAL).  
 FT MOD\_RES 700 700 ALKYLATION (SH-1).  
 FT MOD\_RES 710 710 ALKYLATION (SH-2).  
 FT VARIANT 379 379 G -> D.  
 FT CONFLICT 1547 1547 T -> A (IN REF. 2).  
 FT CONFLICT 1913 1915 ERA -> GRT (IN REF. 2).  
 SQ SEQUENCE 1940 AA; 222816 MW; C348330D75B04DFE2 CRC64;





	Query Match	80.2%	Score	203;	DB	6;	Length	86;
	Best Local Similarity	76.5%;	Pred.	No. 1,3e-17;				
	Matches	39;	Conservative	7;	Mismatches	5;	Indels	0;
					Gaps			0;
OY	1	FVALCAPLAPRDAGSQRP RKEDNVLVSEHSKSLGANKADYNVLTKASQ	51					
		:     :	:	:	:	:	:	
DB	36	FALAPLPFHRDGSQRPRRKEDNVLIESHQSLLEADADVADVYSKTSSQ	86					

SQ	SEQUENCE	1115 AA;	12825 MW;	DA43FABBCB4E2FD9 CRC64;
OY	Query Match		62.5%;	Score 158; DB 11; Length 115;
DB	Best Local Similarity		60.8%;	Pred. No. 6.3e-12;
	Matches 31; Conservative		9; Mismatches 11;	Indels 0; Gaps 0;
	1 FVALGAPLPPRDAGSORPRKKEDNVLVESHESKLGAEAKADVNLTKRSQ 51		11:11 : 1:1 1:1 11:1111: : 1111 : 1111:11:1:1:111	
	65 FVSLSGVOMARDGSHQKPTKKENLVLDGNFRKSLSLEGDKADVLYVKRSQ 115			
RESULT 4				
O9AZW5				
ID	O9AZW5	PRELIMINARY;	PRT:	283 AA.
AC	O9AZW5;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	orf2.			
CN	ORF2.			
OS	bacteriophage phi286.			
OC	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.			
OX	NCBI_TaxID=151536;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
FX	MEDLINE=21113149; PubMed=11160865;			
RA	Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.;			
RT	"Analysis of six prophages in Lactococcus lactis IL1403: different genetic structure of temperate and virulent phage populations.",			
NL	Nucleic Acids Res. 29:644-651(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Chopin A., Sorokin A., Ehrlich S.D., Chopin M.-C.;			
RL	Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL: AF323669; AAK08289.1; -			
SO	SEQUENCE 283 AA; 31164 MW; DE4094313735E02A CRC64;			
Query Match		25.7%;	Score 65; DB 9; Length 283;	
Best Local Similarity		36.1%;	Pred. No. 5.2;	

Oy	15	SQRPKKEDVNLVESHEKSLGKANKADVNLTKAKS	50
		11: :1 :1::11 : :11111111	
Db	110	SKESKSDSNLLIDSOYKEIADENGADSAVLVATKS	145

RESULT 5

QCENFS	ID	QCENFS	PRELIMINARY;	PRT;	283	AA.
AC	09CFN5;					
DT	01-JUN-2001 (TREMBLrel. 17, created)					
DT	01-JUN-2001 (TREMBLrel. 17, last sequence update)					
DT	01-MAR-2002 (TREMBLrel. 20, last annotation update)					
DE	Prophage p13 protein 59.					
GN	p1359 OR LL1432.					
OS	Lactococcus lactis (subsp. lactis) (Streptococcus lactis).					
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;					
OC	Streptococcaceae; Lactococcus.					
OX	NCBI_TaxID=1360;					
XM	[1]					
RM	SEQUENCE FROM N.A.					
RP						
RC	STRAIN-IL1403;					
RX	MEDLINE=21235186; PubMed=11337471;					
RA	Bolotin A., Wincker P., Manger S., Jallion O., Malarne K.,					
RA	Weissenbach J., Ehrlich S.D., Sorokin A.;					
RT	"The complete genome sequence of the lactic acid bacterium Lactococcus					
RT	lactis ssp. lactis IL1403."					
RL	Genome Res. 11:731-753(2001).					
DR	EMBL: AE006373; AAK05530.1; -.					
KM	Complete proteome.					
SO	SEQUENCE	283	AA;	31164	MM;	DF4094313735E02A CRC64;

Query Match 25.7%; Score 65; DB 16; Length 283;

Best Local Similarity 36.1%; Pred. No. 5.2;  
Matches 13; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

OY 15 SORPREKEDNVLSHEKSLGKANKADVNTLTKAKS 50  
DB 110 SKESKSDSNLIDSOYKEIADENGADSAVLATKTS 145

## RESULT 6

023304

ID 023304 PRELIMINARY; PRT: 487 AA.

AC 023304: 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, last sequence update)

DE STE20-like kinase homolog (kinase like protein).

GN ATG14480.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terry N.,

RA Kreis M., Kavanagh T., Entian K.D., Rieger M., James R.,

RA Puigdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A.,

RA Jones J., Palme K., Ansgore W., Delisny M., Bancroft I., Mewes H.W.,

RA Schueller C., Chaiwatiz N.;

RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: 297336; CAB10227.1; -.

DR EMBL: AL161539; CAB78490.1; -.

DR InterPro: IPR000719; Euk.pkinase.

DR InterPro: IPR002290; Ser\_thr.pkinase.

DR Pfam: PF00069; pkinase.1.

DR ProDom: PD000001; Euk.pkinase; 1.

DR SMART: SM00220; S\_TKC.1.

DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.

KW ATP-binding; Transferase.

SQ SEQUENCE 487 AA; 54380 MW; 77D21D39D2F84F20 CRC64;

QY 9 APRDAGSORPREKEDNVLSHEKSLGKANKADVNTLTKAKSQ 51

DB 374 SPREDQSKKKEDNDVITTYGELGIGLSNE-----EAKNQ 409

PRT: 975 AA.

AC 098705: 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)

GN MYOHC-A3 GENE.

OS Notothenia coriiceps (black rockcod).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;

OC Nototheniidae; Notothenia.

OX NCBI\_TaxID=8208;

RN [1]

RP SEQUENCE FROM N.A.

RA Gaurvy L., Ennion S., Ettelaie C., Goldspink G.;

RT "Characterisation of red and white muscle myosin heavy chain gene  
RT coding sequences from Antarctic and tropical fish."

Comp. Biochem. Physiol. 127:575-588(2000).

DR EMBL: A243766; CAC27777.1; -.

DR HSSP: P03437; 1HTM.

DR InterPro: IPR002928; Myosin\_tail.

DR InterPro: IPR000533; Tropomyosin.

DR Pfam: PF01576; Myosin\_tail; 1.

DR PRINTS: PR00194; TROPOMYOSIN.

FT NON\_TER 1 112313 MW; 267AD6A3419537F CRC64;

QY 21 KEDNVLSHEKSLG--EANKADVNTLTKAKSQ 51

DB 34 KEKKALQESHQOTLDDLQAEKDKVNTLTKAKTK 66

PRT: 1119 AA.

AC 097344: 01-MAY-1997 (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)

GN Myosin heavy chain (Fragment).

OS Theragra chalcogramma.

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Acanthomorpha; Paracanthopterygii; Gadiformes; Theragra.

OX NCBI\_TaxID=48550;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=FAST MUSCLE;

RA Togashi M., Hirayama Y., Kakinuma M., Watabe S., Ojima T., Nishita K.;

RT cDNA cloning of Alaska polack fast skeletal muscle myosin heavy

chain.

RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.

DR EMBL: AB000214; BAA19070.1; -.

DR HSSP: P13538; 2MY5.

DR InterPro: IPR002928; Myosin\_tail.

DR Pfam: PF01576; Myosin\_tail; 1.

DR PRINTS: PR00194; TROPOMYOSIN.

FT NON\_TER 1 128626 MW; B8C5FECAE6F5B954 CRC64;

QY 21 KEDNVLSHEKSLG--EANKADVNTLTKAKSQ 51

DB 178 KEKKALQESHQOTLDDLQAEKDKVNTLTKAKTK 210

PRT: 1287 AA.

AC 093498: 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, last annotation update)

GN Myosin heavy chain (Fragment).

OS Theragra chalcogramma.

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Theragra.

OX NCBI\_TaxID=48550;

RN [1]

RP SEQUENCE FROM N.A.

RA Gaurvy L., Ennion S., Ettelaie C., Goldspink G.;







DR InterPro: IPR002928; Myosin\_tail.  
 DR InterPro: IPR002017; Spectrin.  
 DR Pfam: PF00612; IQ; 2.  
 DR Pfam: PF00063; myosin\_head; 1.  
 DR Pfam: PF02736; Myosin\_N; 1.  
 DR Pfam: PF01576; Myosin\_tail; 1.  
 DR ProDom: PD000355; myosin\_head; 1.  
 DR SMART: SM00015; IQ; 1.  
 DR PROSITE: PS50096; IQ; 1.  
 SQ SEQUENCE 1931 AA; 221802 MW; EB57D688E03397D2 CRC64;

Query Match 23.7%; Score 60; DB 13; Length 1931;  
 Best Local Similarity 42.4%; Pred. No. 1.8e+02;  
 Matches 14; Conservative 7; Mismatches 10; Indels 2; Gaps 1;

QY 21 KEDNVLVESHEKSLG--EANKADVNLTKAKSQ 51  
 ||:|||||::||:|||||:  
 DB 989 KEKKILQESHQQLDDLDQAEDKVNPLAKAKGK 1021

Search completed: March 13, 2003, 15:01:52  
 Job time : 21.791 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 13, 2003, 14:52:29 ; Search time 39.6418 Seconds  
(without alignments)  
278.993 Million cell updates/sec

Title: US-09-636-530-2

Sequence: 1 VSEIQLMHNLGKHLNSMERV.....KSLGEANKADVNLTKAKSQ 83

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Gapor 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum DB seq length: 200000000000

Post-processing:	Minimum Match	08
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Listing first 45 summaries

Listing first 45 s

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3:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1982.DAT*
4:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1983.DAT*
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6:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1985.DAT*
7:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1986.DAT*
8:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1987.DAT*
9:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1988.DAT*
10:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1989.DAT*
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12:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1991.DAT*
13:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1992.DAT*
14:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1993.DAT*
15:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1994.DAT*
16:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1995.DAT*
17:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1996.DAT*
18:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1997.DAT*
19:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA1998.DAT*
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22:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA2001.DAT*
23:	/SIDS1/gcgcdatta/geneseq/geneseqp-emb1/AA2002.DAT*

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	422	100.0	84	21	AAB07466	Amino acid sequence
2	418	99.1	82	21	AAB07465	Amino acid sequence
3	417	98.8	84	13	AAR23790	Parathyroid hormone
4	417	98.8	84	13	AAR25571	Human PTH encoded
5	417	98.8	84	14	AAR42067	Human PTH encoded
6	417	98.8	84	17	AAW29420	Human parathyroid
7	417	98.8	84	17	AAW29420	Human parathyroid
8	417	98.8	84	18	AAW25780	Target peptide (PTH)
9	417	98.8	84	20	AAV02577	Human parathyroid
10	417	98.8	84	22	AAB91082	Human parathyroid hormone

11	417	98.8	84	23	AAE23726	Human parathyroid
12	417	98.8	84	23	ABB08594	Human parathyroid
13	417	98.8	84	23	AAE18392	Human PTH peptide
14	417	98.8	84	23	AAE14316	Salmon calcitonin
15	417	98.8	84	23	AAU73022	Parathyroid hormone
16	417	98.8	115	5	AAp40251	Protein sequence 1
17	417	98.8	115	9	AAp80305	Sequence of human
18	417	98.8	115	9	AAp80275	Sequence of human
19	417	98.8	115	16	AAp75693	Human prepro-PTH.
20	414	98.1	84	13	AAp28846	Oxidation resistant
21	414	98.1	84	13	AAp28847	Oxidation resistant
22	414	98.1	84	14	AAp30857	Leu18 hPTH mutcin.
23	413	97.9	84	14	AAp42068	Stability-enhanced
24	412	97.6	84	14	AAp30856	Cys35 hPTH mutcin.
25	412	97.6	84	14	AAp42070	Stability-enhanced
26	412	97.6	84	17	AAp99448	Human parathyroid
27	411	97.4	84	13	AAp28845	Oxidation resistant
28	411	97.4	84	13	AAp28847	Oxidation resistant
29	411	97.4	84	13	AAp29562	Oxidation resistant
30	411	97.4	84	14	AAp42071	Stability-enhanced
31	411	97.4	84	15	AAp49692	Sequence of varian
32	411	97.4	84	15	AAp49693	Sequence of varian
33	411	97.4	84	15	AAp49694	Sequence of varian
34	410	97.2	84	13	AAp29564	Oxidation resistant
35	410	97.2	84	13	AAp29565	Oxidation resistant
36	410	97.2	84	14	AAp42069	Stability-enhanced
37	410	97.2	84	15	AAp49696	Sequence of varian
38	409	96.9	81	14	AAp30854	hPTH mutcin lackin
39	409	96.9	84	13	AAp21155	Human parathyroid
40	409	96.9	84	13	AAp23338	Human parathyroid
41	409	96.9	84	13	AAp23339	Human parathyroid
42	409	96.9	84	13	AAp23344	Human parathyroid
43	409	96.9	84	13	AAp21250	Human parathyroid
44	409	96.9	84	13	AAp21251	Human parathyroid
45	409	96.9	84	13	AAp21256	Human parathyroid

## ALIGNMENTS

XX	RESULT 1
XX	AAB07464
ID	AAB07464 standard; protein; 84 AA.
AC	AAB07464;
DT	20-OCT-2000 (first entry)
DE	Amino acid sequence of human parathyroid hormone.
XX	Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
XX	Homo sapiens.
OS	
PN	WO200042437-A1.
PD	20-JUL-2000.
PF	13-JAN-2000; 2000WO-US00855.
PR	14-JAN-1999; 99US-0231422.
PR	26-JUN-1999; 99US-0344639.
PA	(SCAN-) SCANTIBODIES LAB INC.
DR	WPI; 2000-476147/41.
PT	Differentiating between normal parathyroid function and
PT	hyperparathyroidism comprises determining and comparing whole
PT	parathyroid hormone, parathyroid hormone inhibitory peptide fragment
PT	and/or total parathyroid hormone levels -
SS	Disclosure; Fig 1; 46pp; English.

XX The present sequence represents a human parathyroid hormone (PTH).  
 CC Fragments of PTH function as PTH antagonists. The specification  
 CC describes a method for differentiating between a person having  
 CC substantially normal parathyroid function and having hyperparathyroidism.  
 CC The method comprises determining and comparing at least two of the  
 CC following parameters: whole parathyroid hormone level, parathyroid  
 CC hormone inhibitory peptide fragment level and total parathyroid hormone  
 CC level. The method is used for monitoring (treatments of) parathyroid  
 CC related bone disease and the effects of therapeutic treatment for  
 CC hyperparathyroidism.  
 XX

Sequence 84 AA:

Query Match 100.0%; Score 422; DB 21; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 5e-42;  
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIQLMHNLGKHLNSMEREWMLRKLDVHNHVALGAPLAPRDAGSQRPKKEDNVLYE 60  
 DB 2 VSEIQLMHNLGKHLNSMEREWMLRKLDVHNHVALGAPLAPRDAGSQRPKKEDNVLYE 61  
 OY 61 SHEKSLGEANKADVNVLTAKSQ 83  
 DB 62 SHEKSLGEANKADVNVLTAKSQ 84

# RESULT 2

AAB07465  
 ID AAB07465 standard; protein; 82 AA.

AC AAB07465;

DT 20-OCT-2000 (first entry)

XX Amino acid sequence of human parathyroid hormone antagonist.

XX Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.

OS Homo sapiens.

XX WO200042437-A1.

XX 20-JUL-2000.

XX 13-JAN-2000; 2000WO-US00855.

XX 14-JAN-1999; 99US-0231422.

XX 26-JUN-1999; 99US-0344639.

XX (SCAN-) SCANTIBODIES LAB INC.

XX WPI: 2000-476147/41.

DR Differentiating between normal parathyroid function and  
 PT hyperparathyroidism comprises determining and comparing whole  
 PT parathyroid hormone, parathyroid hormone inhibitory peptide fragment  
 PT and/or total parathyroid hormone levels -  
 XX

PS Disclosure: Page 42-43; 46pp; English.

XX The present sequence represents a fragment of human parathyroid  
 CC hormone (PTH), comprising residues 3-84, which functions as a PTH  
 CC antagonist. The specification describes a method for differentiating  
 CC between a person having substantially normal parathyroid function  
 CC and having hyperparathyroidism. The method comprises determining and  
 CC comparing at least two of the following parameters: whole parathyroid  
 CC hormone level, parathyroid hormone inhibitory peptide fragment level  
 CC and total parathyroid hormone level. The method is used for monitoring  
 CC (treatments of) parathyroid related bone disease and the effects of  
 CC therapeutic treatment for hyperparathyroidism.  
 XX

Sequence 82 AA:

Query Match 99.1%; Score 418; DB 21; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEIQLMHNLGKHLNSMEREWMLRKLDVHNHVALGAPLAPRDAGSQRPKKEDNVLYE 61  
 DB 1 SEIQLMHNLGKHLNSMEREWMLRKLDVHNHVALGAPLAPRDAGSQRPKKEDNVLYE 60  
 OY 62 HEKSLGEANKADVNVLTAKSQ 83  
 DB 61 HEKSLGEANKADVNVLTAKSQ 82

# RESULT 3

AAR23790  
 ID AAR23790 standard; protein; 84 AA.

XX AAR23790;

DT 03-NOV-1992 (first entry)

XX Parathyroid hormone gene product.

XX hPTH; hypoparathyroidism; osteoporosis.

OS Synthetic.

XX EP483509-A.

XX 06-MAY-1992.

XX 25-SEP-1991; 91EP-0116281.

XX 28-SEP-1990; 90JP-0257491.

XX 20-MAR-1991; 91JP-0056434.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Fukuda T, Oshika Y, Yamada T;

XX WPI: 1992-152248/19.

XX N-PSDB: AAQ24478.

XX Synthetic gene encoding human parathyroid hormone - formed by  
 PT ligating oligo-nucleotide(s) and expressed at high yield in E  
 PT coli  
 XX

PS Disclosure: Page 21; 33pp; English.

XX The human parathyroid hormone (hPTH) sequence given is the product of  
 CC a synthetic gene which corresponds to the amino acid sequence of hPTH.  
 CC The DNA sequence was produced by enzymatically ligating  
 CC oligodeoxynucleotides. hPTH is an important regulator of calcium  
 CC metabolism and has clinical applications. to diseases such as  
 CC hypoparathyroidism and osteoporosis. This hPTH can be used as a  
 CC therapeutic agent or to study the biological role of hPTH in vivo.  
 XX

Sequence 84 AA:

Query Match 98.8%; Score 417; DB 13; Length 84;  
 Best Local Similarity 98.8%; Pred. No. 1.9e-41;  
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIQLMHNLGKHLNSMEREWMLRKLDVHNHVALGAPLAPRDAGSQRPKKEDNVLYE 60  
 DB 2 VSEIQLMHNLGKHLNSMEREWMLRKLDVHNHVALGAPLAPRDAGSQRPKKEDNVLYE 61  
 OY 61 SHEKSLGEANKADVNVLTAKSQ 83  
 DB 62 SHEKSLGEANKADVNVLTAKSQ 84

```

RESULT 4
AAR25571
ID AAR25571 standard; Protein; 84 AA.
XX
XX
AC AAR25571;
XX
DT 13-JAN-1993 (first entry)
XX
DE Human PTH encoded by px.
XX
KW Parathyroid; hormone; osteoporosis; psoriasis; oxidation;
KM resistance.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 8 /note= "see CC"
FT Misc-difference 18
FT /note= "see CC"
XX
XX
PN W09211286-A.
XX
PD 09-JUL-1992.
XX
PF 18-DEC-1991; 91WO-CA00451.
XX
PR 21-DEC-1990; 90US-0630969.
PR 13-DEC-1991; 91US-0806271.
XX
PA (ALILE-) ALLELIX BIOPHARMACEUTICALS INC.
PA (GLAX ) GLAXO CANADA INC.
XX
PI Bozatto RP, Kronis KA;
XX
DR WPI; 1992-250028/30.
DR N-PSDB; AAO26498.
XX
XX
PT New oxidn. resistant variants of parathyroid hormone - used for
treatng osteoporosis, psoriasis and cardiovascular disorders
XX
PS Disclosure; Fig 1; 40pp; English.
XX
CC Variants of PTH exhibiting PTH activity and reduced sensitivity
to oxidation are obtained by replacing at least one Met residue in
PTH (positions 8 and 18) with a genetically encoded amino acid,
other than Met and Cys.
CC The Met amino acids are indicated in the Features Table.
CC The variant may be obtd. using recombinant technique, and may be
used for treating osteoporosis, other bone-related disorders,
psoriasis and cardiovascular disorders.
CC Human PTH refers to the mature form of the hormone, which consists
of 84 amino acids arranged in the sequence reported by Kimura et al,
CC 1993, Biochem. Biophys. Res. Comm., 114(2):493.
CC Examples of variants are given in AAR28845-48 and AAR29561-69.
XX
SQ . Sequence 84 AA;

Query Match 98.8%; Score 417; DB 13; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.9e-41;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIOLMNLGKHLNLSMEVEWLRKKLDVHNFFVALGAPLARDGSGRPKRKEDNVLYE 60
DB 2 VSEIOLMNLGKHLNLSMEVEWLRKKLDVHNFFVALGAPLARDGSGRPKRKEDNVLYE 60
OY 61 SHEKSLGEANKADVNVLTAKSQ 83
DB 62 SHEKSLGEADKADVNVLTAKSQ 84

RESULT 5
AAR42067

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ID AAR42067 standard; Protein; 84 AA.
XX
XX
AC AAR42067;
XX
DT 05-MAY-1994 (first entry)
XX
DE Human parathyroid hormone.
XX
KW PTH; hPTH; stability-enhanced; mutant; resistance; proteolytic;
KM enzymes; osteoporosis; bone-related disorders.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 25..27 /note= "Arglysls which may be mutated"
XX
XX
PN W09320203-A.
XX
PD 14-OCT-1993.
XX
PF 31-MAR-1993; 93WO-CA00136.
XX
PR 03-APR-1992; 92US-0863014.
XX
PA (ALILE-) ALLELIX BIOPHARMACEUTICALS INC.
PA (GLAX ) GLAXO CANADA INC.
XX
PI Bozatto RP, Kronis KA;
XX
DR WPI; 1993-336911/42.
DR N-PSDB; AAO49955.
XX
XX
PT New parathyroid hormone variants - having aminoacid replacements
at positions 25 to 27 to enhance resistance to proteolytic
enzymes;
XX
PS Disclosure; Fig 2; 44pp; English.
XX
CC The sequence is that of human parathyroid hormone (hPTH) which
may be mutated in the region Arg25Lys26Lys27 to provide variants
CC with enhanced stability in the presence of proteolytic enzymes
such as trypsin.
XX
SQ . Sequence 84 AA;

Query Match 98.8%; Score 417; DB 14; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.9e-41;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIOLMNLGKHLNLSMEVEWLRKKLDVHNFFVALGAPLARDGSGRPKRKEDNVLYE 60
DB 2 VSEIOLMNLGKHLNLSMEVEWLRKKLDVHNFFVALGAPLARDGSGRPKRKEDNVLYE 61
OY 61 SHEKSLGEANKADVNVLTAKSQ 83
DB 62 SHEKSLGEADKADVNVLTAKSQ 84

RESULT 6
AAM29420
ID AAM29420 standard; Protein; 84 AA.
XX
XX
AC AAM29420;
XX
DT 24-FEB-1998 (first entry)
XX
DE Human parathyroid hormone.
XX
KW Parathyroid hormone; PTH; osteoporosis; inhalation; pulmonary;
KM bone formation.
XX
OS Homo sapiens.

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XX  XX  WO9619206-A1.
XX  XX  27-JUN-1996.
XX  XX  08-DEC-1995; 95WO-SE01475.
XX  XX  12-JUL-1995; 95SE-0002576.
XX  XX  22-DEC-1994; 94SE-0004449.
XX  XX  (ASTR ) ASTRA AB.
XX  XX  Backstrom K, Wallmark B;
XX  XX  WPI: 1996-309285/31.
XX  XX  Composition for administration by inhalation to treat osteoporosis
XX  XX  and stimulate bone formation - comprises parathyroid hormone in form
XX  XX  of dry powder mainly of particle size below 10 microns
XX  XX  Claim 9; Pages 15-16; 25pp; English.
XX  XX  The present sequence represents human parathyroid hormone which is used
XX  XX  in a new therapeutic preparation for the treatment of osteoporosis.
XX  XX  The active substance is in the form of a dry powder suitable for
XX  XX  inhalation, in which at least 50% of the dry powder consists of particles
XX  XX  of up to 10 microns in diameter or agglomerates of such particles.
XX  XX  Pulmonary administration of the parathyroid hormone is effective in the
XX  XX  stimulation of bone formation.
XX  XX  Sequence 84 AA;

Query Match          98.8%; Score 417; DB 17; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.9e-41;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY  1 VSEIQLMHNIGKHLNSMEREWMLRKLDQVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
DB  2 VSEIQLMHNIGKHLNSMEREWMLRKLDQVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 61
OY  61 SHEKSLGEANKADVNVLTKAKSQ 83
DB  62 SHEKSLGEADKADVNVLTKAKSQ 84

RESULT 7
AAR98954
ID  AAR98954 standard; peptide; 84 AA.
XX  XX  AAR98954;
XX  XX  15-JAN-1997 (first entry)
XX  XX  Target peptide (PTH(1-84)) used in fusion protein construct.
XX  XX  Fusion protein construct; isolation; purification;
XX  XX  growth hormone releasing factor; glucagon-like peptide 1;
XX  XX  parathyroid hormone; inclusion body; carbonic anhydrase.
XX  XX  Synthetic.
XX  XX  WO9617942-A1.
XX  XX  13-JUN-1996.
XX  XX  07-DEC-1995; 95WO-US15800.
XX  XX  07-DEC-1994; 94US-0350530.
XX  XX  (BION-) BIONEBRASKA INC.
XX  XX  De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;
XX  XX  Partridge BE, Stout JS, Wagner FW;

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XX  XX  WPI: 1996-287186/29.
XX  XX  Isolation and purification of peptide(s) from fusion protein constructs
XX  XX  PT - which include a carbonic anhydrase and a variable fused
XX  XX  polypeptide
XX  XX  Claim 58; Page 49; 67pp; English.
XX  XX  A new method for the isolation and/or purification of a recombinant
XX  XX  CC peptide employs a fusion protein construct (FPC) comprising a
XX  XX  CC carbonic anhydrase and a variable fused polypeptide containing a
XX  XX  CC target peptide. The method comprises precipitating either the FPC or
XX  XX  CC a fragment of the FPC including the carbonic anhydrase. An
XX  XX  CC alternative method of producing the peptide comprises expressing the
XX  XX  CC FPC as part of an inclusion body. The target peptides of the FPC are
XX  XX  CC derived from growth hormone releasing factor (GRF), glucagon-like
XX  XX  CC peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence
XX  XX  CC corresponds to amino acids 1-84 of PTH.
XX  XX  Sequence 84 AA;

Query Match          98.8%; Score 417; DB 17; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.9e-41;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY  1 VSEIQLMHNIGKHLNSMEREWMLRKLDQVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
DB  2 VSEIQLMHNIGKHLNSMEREWMLRKLDQVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 61
OY  61 SHEKSLGEANKADVNVLTKAKSQ 83
DB  62 SHEKSLGEADKADVNVLTKAKSQ 84

RESULT 8
AAW25687
ID  AAW25687 standard; Peptide; 84 AA.
XX  XX  AAW25687;
XX  XX  14-APR-1998 (first entry)
XX  XX  Human parathyroid hormone peptide hPTH (residues 1-84).
XX  XX  Kex2 protease; derivative; cleave; yeast; enzyme; chimeric protein;
XX  XX  human; parathyroid hormone peptide; hPTH.
XX  XX  Homo sapiens.
XX  XX  Key Location/Qualifiers
XX  XX  FH Cleavage-site 43..44 "cleaved by Kex2 protease"
XX  XX  FT Cleavage-site 51..52 /note="cleaved by Kex2 protease"
XX  XX  FT
XX  XX  PN EP794254-A2.
XX  XX  PD 10-SEP-1997.
XX  XX  PF 04-MAR-1997; 97EP-0301429.
XX  XX  PR 16-DEC-1996; 96JP-0352580.
XX  XX  PR 04-MAR-1996; 96JP-0073217.
XX  XX  PA (SUNR ) SUNTORY LTD.
XX  XX  Magota K, Masuda T, Suzuki Y, Yabuta M;
XX  XX  WPI: 1997-437479/41.
XX  XX  Secreted forms of Kex2 protease - useful for cleaving chimeric
XX  XX  PT proteins

```

XX PS Disclosure: Page 25; 82pp; English.

CC CC This is the human parathyroid hormone peptide hPTH (residues 1-84). This

CC CC is used in the construction of a chimeric protein betagal-139S(FM)PPH84.

CC CC The enzyme Kex2 protease can be used for excision of a desired protein

CC CC from a chimeric protein comprising the desired protein and an Arg-Arg,

CC CC Lys-Arg or Pro-Arg sequence adjacent to the N terminus of the desired

CC CC protein. It can be specifically used for cleaving this human parathyroid

CC CC hormone peptide hPTH(1-84) or peptide hPTH(1-34) from chimeric proteins

CC CC such as the beta Gal-139S(FM)PPH84 or CATPH34. Derivatives of Kex2

CC CC protease, and especially Kex2-660 can also cleave such chimeric proteins

CC CC with high specificity and efficiency even in the absence of urea.

XX SQ Sequence 84 AA:

Query Match 98.8%; Score 417; DB 18; Length 84;

Best Local Similarity 98.8%; Pred. No. 1.9e-41;

Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIOLMHLGKHLMSMERVEWLRKKLDVHNFVALGAPLARDGSGRPKKEDNVLYE 60

DB 2 VSEIOLMHLGKHLMSMERVEWLRKKLDVHNFVALGAPLARDGSGRPKKEDNVLYE 61

OY 61 SHEKSLGEANKADVNVLTAKSQ 83

DB 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 9

AA02577

ID AA02577 standard; protein; 84 AA.

AC AAY02577;

XX 16-JUL-1999 (first entry)

XX DE Human parathyroid hormone (hPTH) protein.

XX DE Human parathyroid hormone; hPTH; bone mass;

XX KM 3-(substituted phenoxy)benzo(b)thiophene compound;

XX KM bone loss treatment; osteoporosis.

XX OS Homo sapiens.

XX PN WO9918945-A1.

XX PD 22-APR-1999.

XX PF 05-OCT-1998; 98WO-US20848.

XX PR 14-OCT-1997; 97US-0061800.

XX PA (ELIL ) LILLY & CO ELI.

XX PI Sato M;

XX DR WPI: 1999-287871/24.

XX PT Method of building bone mass by co-administration of a parathyroid

XX PT hormone with a 3-(substituted phenoxy)benzo(b)thiophene compound

XX PS Claim 5; Page 38; 48pp; English.

XX CC The present sequence represents human parathyroid hormone (hPTH). It,

XX CC and its fragments, are used in the method of the invention. The

XX CC specification describes a method for building bone mass, comprising

XX CC coadministration of a parathyroid hormone with a 3-(substituted

XX CC phenoxy)benzo(b)thiophene compound. The method is used for treatment

XX CC of bone loss, e.g. in osteoporosis.

XX SQ Sequence 84 AA;

Query Match 98.8%; Score 417; DB 20; Length 84;

Best Local Similarity 98.8%; Pred. No. 1.9e-41;

Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIOLMHLGKHLMSMERVEWLRKKLDVHNFVALGAPLARDGSGRPKKEDNVLYE 60

DB 2 VSEIOLMHLGKHLMSMERVEWLRKKLDVHNFVALGAPLARDGSGRPKKEDNVLYE 61

OY 61 SHEKSLGEANKADVNVLTAKSQ 83

DB 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 10

AAB91082

ID AAB91082 standard; Peptide; 84 AA.

AC AAB91082;

XX 22-JUN-2001 (first entry)

XX DE Parathyroid hormone (PTH) related peptide SEQ ID NO:256.

XX KM Protection; endogenous therapeutic peptide; peptidase; conjugation;

XX KM blood component; modification; succinimidyl; maleimido group; amino;

XX KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US33576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1998; 98US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thiabaudau K;

XX DR WPI: 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents

XX PT peptidase degradation, useful for increasing length of in vivo activity

XX PS Disclosure: Page 274-275; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)

XX CC comprising a therapeutically active amino acid region (III) and a

XX CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to

XX CC a less therapeutically active amino acid region (IV), which covalently

XX CC bonds with amino/hydroxyl/thiol groups on blood components to form a

XX CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

XX CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

XX CC factors and neurotransmitters, to protect them from peptidase activity

XX CC in vivo for the treatment of various disorders. Endogenous therapeutic

XX CC peptides are not suitable as drug candidates as they require frequent

XX CC administration due to rapid degradation by peptidases in the body.

XX CC Modifying and attaching therapeutic peptides to albumin prevents or

XX CC reduces the action of peptidases to increase length of activity (half

XX CC life) and specificity as bonding to large molecules decreases

XX CC intracellular uptake and interference with physiological processes.

XX CC AAB90829 to AAB92441 represent peptides which can be used in the

XX CC exemplification of the present invention.

XX SQ Sequence 84 AA;

Query Match 98.8%; Score 417; DB 22; Length 84;

Best Local Similarity 98.8%; Pred. No. 1.9e-41;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIQLMHNIGKHLNSMERVEWLRKKLDVHNFEVALGAPLAPRDAGSQRRPKKEDNVLYE 60  
|||||:|||||  
DB 2 VSEIQLMHNIGKHLNSMERVEWLRKKLDVHNFEVALGAPLAPRDAGSQRRPKKEDNVLYE 61

OY 61 SHEKSLGEANKADVNVLTAKSQ 83  
|||||:|||||  
DB 62 SHEKSLGEADKADVNVLTAKSQ 84

RESULT 11  
AAE23726  
ID AAE23726 standard; peptide; 84 AA.  
XX  
AC AAE23726;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Human parathyroid hormone (hPTH) peptide (1-84).  
XX  
KM Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;  
KM hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;  
KM acne; actinic keratosis; alopecia; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200228420-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 05-OCT-2001; 2001WO-US31082.  
XX  
PR 06-OCT-2000; 2000US-238134P.  
XX  
PA (HOLI/) HOLICK M F.  
XX  
PI Holick MF;  
XX  
DR WPI: 2002-452304/48.  
DR N-PSDB; AAD37995.  
XX  
PT Regulating mammalian skin or hair cell proliferation and  
PT differentiation by administering nucleic acids encoding peptides  
PT derived from N-terminal region of human parathyroid hormone (hPTH) or  
PT hPTH-related protein -  
XX  
PS Claim 5; Fig 18; 56pp; English.  
XX  
CC The invention relates to a method for regulating proliferation or  
CC enhancing differentiation of mammalian skin or hair cell. The method  
CC involves administering nucleic acids encoding peptides derived from  
CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related  
CC peptide (PTHrP). The method is used for inhibiting hyperproliferative  
CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic  
CC keratosis, skin cancer, for inhibiting hair growth or preventing hair  
CC regrowth. It is useful for stimulating cell growth, rejuvenating aged  
CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound  
CC healing, stimulating hair growth, maintaining hair growth, treating or  
CC preventing female or male pattern baldness, for treating chemotherapy  
CC induced alopecia and also for stimulating epidermal cell growth or  
CC hair follicle cell growth. The method is also used in gene therapy.  
CC  
XX  
SQ Sequence 84 AA;

Query Match 98.8%; Score 417; DB 23; Length 84;  
Best Local Similarity 98.8%; Pred. No. 1.9e-41;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIQLMHNIGKHLNSMERVEWLRKKLDVHNFEVALGAPLAPRDAGSQRRPKKEDNVLYE 60  
|||||:|||||

DB 2 VSEIQLMHNIGKHLNSMERVEWLRKKLDVHNFEVALGAPLAPRDAGSQRRPKKEDNVLYE 61

OY 61 SHEKSLGEANKADVNVLTAKSQ 83  
|||||:|||||  
DB 62 SHEKSLGEADKADVNVLTAKSQ 84

RESULT 12  
ABB08594  
ID ABB08594 standard; protein; 84 AA.  
XX  
AC ABB08594;  
XX  
DT 23-MAY-2002 (first entry)  
XX  
DE Human parathyroid hormone.  
XX  
KM Human; parathyroid hormone; hPTH; osteopathic.  
XX  
OS Homo sapiens.  
XX  
PN WO200202136-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 29-JUN-2001; 2001WO-JP05674.  
XX  
PR 30-JUN-2000; 2000JP-0237717.  
PR 30-JUN-2000; 2000JP-0237718.  
XX  
PA (SUNR ) SUNTORY LTD.  
XX  
PI Minamitake Y, Ono T, Kawanishi K, Suzuki Y;  
XX  
DR WPI: 2002-147974/19.  
XX  
PT Drug compositions for nasal administration comprising human parathyroid  
PT hormone peptide or its derivative and acetic acid, is applicable for  
PT long-term therapy of osteoporosis -  
XX  
PS Claim 3; Page 64; 67pp; Japanese.  
XX  
CC This invention relates to components comprising of human parathyroid  
CC hormone peptide (hPTH) and less than their stoichiometric equivalent  
CC of acetic acid. The compositions are applicable for long-term therapy  
CC of osteoporosis. The present sequence represents human parathyroid  
CC hormone.  
XX  
SQ Sequence 84 AA;

Query Match 98.8%; Score 417; DB 23; Length 84;  
Best Local Similarity 98.8%; Pred. No. 1.9e-41;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIQLMHNIGKHLNSMERVEWLRKKLDVHNFEVALGAPLAPRDAGSQRRPKKEDNVLYE 60  
|||||:|||||  
DB 2 VSEIQLMHNIGKHLNSMERVEWLRKKLDVHNFEVALGAPLAPRDAGSQRRPKKEDNVLYE 61

OY 61 SHEKSLGEANKADVNVLTAKSQ 83  
|||||:|||||  
DB 62 SHEKSLGEADKADVNVLTAKSQ 84

RESULT 13  
AAE18392  
ID AAE18392 standard; peptide; 84 AA.  
XX  
AC AAE18392;  
XX  
DT 07-MAY-2002 (first entry)  
XX  
DE Human PTH peptide #5.  
XX



KM Human; cell proliferation; cell differentiation; parathyroid hormone;  
 KW PTH; parathyroid related peptide; hyperproliferative skin disorder;  
 KW psoriasis; ichthyosis; actinic keratosis; alopecia; skin cell growth;  
 KW hair growth; wrinkle; wound healing; chemotherapy; skin cancer; PTHrP.  
 OS Homo sapiens.  
 XX WO200198348-A2.  
 PN  
 XX  
 XX 27-DEC-2001.  
 PD  
 XX  
 XX 20-JUN-2001; 2001WO-US19650.  
 PF  
 XX  
 XX 22-JUN-2000; 2000US-213247P.  
 PR  
 XX  
 XX (HOLL) HOLICK M F.  
 PA  
 XX  
 XX Holick MF;  
 PI  
 XX  
 XX WPI; 2002-171552/22.  
 DR  
 XX  
 XX  
 XX Modulating proliferation or differentiation of mammalian skin or hair  
 PT cell for treating hyperproliferative diseases, comprises topical  
 PT administration of liposome encapsulated-peptide identical to  
 PT parathyroid hormone -  
 XX  
 XX  
 XX Disclosure: Page 10; 58pp; English.  
 PS  
 XX  
 XX The invention relates to a method of modulating proliferation or  
 CC differentiation of mammalian skin or hair cell. The method involves  
 CC topical administration of a liposome encapsulated-peptide, its salt  
 CC or derivative, identical to parathyroid hormone (PTH) or parathyroid  
 CC related peptide (PTHrP). Method of the invention is useful for  
 CC inhibiting hyperproliferative skin disorders e.g. psoriasis,  
 CC ichthyosis, actinic keratosis, skin cancer, inhibiting hair growth or  
 CC preventing hair regrowth. It is also useful for stimulating skin cell  
 CC growth, rejuvenating aged skin, preventing and treating skin wrinkles,  
 CC enhancing wound healing, stimulating hair growth, maintaining hair  
 CC growth, treating or preventing female or male pattern baldness,  
 CC treating chemotherapy induced alopecia and for stimulating epidermal  
 CC cell growth and hair follicle cell growth. The present sequence is  
 CC human PTH peptide used in the method of the invention.  
 CC  
 XX  
 XX Sequence 84 AA:  
 SQ  
 Query Match 98.8%; Score 417; DB 23; Length 84;  
 Best Local Similarity 98.8%; Pred. No. 1.9e-41;  
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 VSEIOLMHNLGKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVIVE 60  
 DB 2 VSEIOLMHNLGKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVIVE 61  
 OY 61 SHEKSLGEADKADVNVLTAKSQ 83  
 DB 62 SHEKSLGEADKADVNVLTAKSQ 84  
 RESULT 14  
 AAEI4316  
 ID AAEI4316 standard; Protein; 84 AA.  
 AC  
 XX AAEI4316;  
 AC  
 XX  
 XX 07-MAR-2002 (first entry)  
 DT  
 XX  
 XX Salmon calcitonin (CT) receptor modulating domain.  
 DE  
 XX  
 XX Calcitonin; CT; CT receptor; Fc domain; therapy; osteoporosis;  
 KW osteopathic; salmon.  
 KW  
 XX  
 XX Oncorhynchus sp.  
 OS  
 XX

PN WO200183526-A2.  
 XX  
 XX 08-NOV-2001.  
 PD  
 XX  
 XX 03-MAY-2001; 2001WO-US14320.  
 PF  
 XX  
 XX 03-MAY-2000; 2000US-201511P.  
 PR  
 XX 02-MAY-2001; 2001US-0847712.  
 PR  
 XX  
 XX (AMGE-) AMGEN INC.  
 PA  
 XX  
 XX Liu C, Marshall WS, Reynolds A;  
 PI  
 XX  
 XX WPI; 2002-034503/04.  
 DR  
 XX  
 XX Compositions comprising Calcitonin receptor modulator domains, useful  
 PT for treating osteoporosis -  
 PT  
 XX  
 XX Claim 14; Page 17; 64pp; English.  
 PS  
 XX  
 XX The invention relates to therapeutic agents that modulate the  
 CC activity of calcitonin (CT) receptor. Modulators of CT receptor  
 CC comprise a CT receptor modulating domain and a vehicle such as a  
 CC polymer or an Fc domain, where the vehicle is covalently attached  
 CC to the CT receptor modulating domain. The compositions comprising  
 CC CT receptor modulating domains are used to treat osteoporosis.  
 CC The present sequence is salmon calcitonin receptor modulating domain.  
 CC  
 XX  
 XX Sequence 84 AA:  
 SQ  
 Query Match 98.8%; Score 417; DB 23; Length 84;  
 Best Local Similarity 98.8%; Pred. No. 1.9e-41;  
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 VSEIOLMHNLGKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVIVE 60  
 DB 2 VSEIOLMHNLGKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVIVE 61  
 OY 61 SHEKSLGEADKADVNVLTAKSQ 83  
 DB 62 SHEKSLGEADKADVNVLTAKSQ 84  
 RESULT 15  
 AAU73022  
 ID AAU73022 standard; Peptide; 84 AA.  
 AC  
 XX AAU73022;  
 AC  
 XX  
 XX 12-MAR-2002 (first entry)  
 DT  
 XX  
 XX Parathyroid hormone PTH/PTHrP modulating domain #4.  
 DE  
 XX  
 XX Human; parathyroid hormone; PTH; parathyroid hormone-related protein;  
 KW PTHrP; bone resorption inhibitor; osteoprotegerin; OPG; OPG-L antibody;  
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;  
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;  
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;  
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;  
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;  
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;  
 KW immunoglobulin G; IgG.  
 KW  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200181415-A2.  
 PN  
 XX  
 XX 01-NOV-2001.  
 PD  
 XX  
 XX 27-APR-2001; 2001WO-US13528.  
 PF  
 XX  
 XX 27-APR-2000; 2000US-200053P.  
 PR  
 XX 28-JUN-2000; 2000US-214860P.  
 PR

PR 06-FEB-2001; 2001US-266673P.  
PR 26-APR-2001; 2001US-0843221.

XX  
XX  
PA (AMGE-) AMGEN INC.

PI Kostenuik P, Liu C, Lacey DL;  
XX  
XX

DR MPI; 2002-066435/09.

XX  
XX  
PT Composition, useful for treating osteopenia, comprises parathyroid  
PT hormone and parathyroid hormone-related protein receptor modulators -  
XX

PS Disclosure; Page 25; 107pp; English.

XX  
XX  
CC The invention relates to a composition (I) comprising modulators of  
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)  
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)  
CC comprising PTH agonist optionally with a bone resorption inhibitor, such  
CC as osteoprotegerin (OPG), OPG-L antibody, calcitonin, bisphosphonates,  
CC oestrogens, oestrogen receptor modulators and tibolone is useful for  
CC treating osteopenia. (I) is useful for therapeutic and prophylactic  
CC purposes. Antagonists of PTH receptor are useful in treating primary and  
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,  
CC particularly breast and prostate cancer, cachexia and anorexia,  
CC osteopenia, including various forms of osteoporosis, Paget's disease of  
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with  
CC traumatic injury or nontraumatic necrosis associated with Gaucher's  
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid  
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are  
CC useful as therapeutic agents in conditions including fracture repair  
CC (including healing of non-union fractures), osteopenia, including various  
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone  
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and  
CC related amino acid sequences of the invention.  
XX

SQ Sequence 84 AA;

Query Match 98.8%; Score 417; DB 23; Length 84;  
Best Local Similarity 98.8%; Pred. No. 1.9e-41;

Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMEREMLRKKQDYHNFFALGAPLAPRAGSQRRKKEDNVLE 60  
DB 2 VSEIQLMHNIGKHLNSMEREMLRKKQDYHNFFALGAPLAPRAGSQRRKKEDNVLE 61

QY 61 SHEKSLGEANKADYNVLTAKASQ 83  
DB 62 SHEKSLGEADKADYNVLTAKASQ 84

Search completed: March 13, 2003, 15:00:25  
Job time : 40.6418 secs

GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: March 13, 2003, 14:46:09 ; Search time 14.2463 Seconds  
(without alignments)  
171.421 Million cell updates/sec

Title: US-09-636-530-2

Perfect score: 422

Sequence: 1 VSEIQLMNLGKHLNSMERV.....KSLGEANKADVNLTKAKSQ 83

Scoring table:

BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued\_Patents\_AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PTCUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417	98.8	84	1	US-07-863-014-2
2	417	98.8	84	1	US-08-332-453-2
3	417	98.8	84	1	US-08-689-190-2
4	417	98.8	84	2	US-08-835-231-9
5	417	98.8	84	2	US-08-805-918-3
6	417	98.8	84	4	US-09-108-661-9
7	417	98.8	84	5	PCT-US95-15800-25
8	412	97.6	84	2	US-08-142-551B-1
9	412	97.6	84	2	US-08-411-726-1
10	407	96.4	84	1	US-07-707-114-1
11	368	87.2	84	1	US-07-773-098-2
12	364	86.3	84	2	US-08-733-446-5
13	359	85.1	84	1	US-07-773-098-1
14	356	84.4	81	2	US-08-733-446-4
15	352	83.4	81	2	US-07-776-272-14
16	351	83.2	80	2	US-08-733-446-3
17	350	82.9	84	1	US-07-773-098-9
18	350	82.9	84	1	US-07-773-098-10
19	347	81.0	78	2	US-08-733-446-2
20	342	81.0	79	2	US-08-733-446-1
21	341	80.8	84	1	US-07-773-098-7
22	341	80.8	84	1	US-07-773-098-8
23	337	79.9	84	3	US-09-044-536A-36
24	248	58.8	51	3	US-09-044-536A-7
25	237	56.2	50	2	US-08-142-551B-119
26	193	45.7	38	1	US-08-112-024-1
27	193	45.7	38	1	US-08-232-849-1

28	193	45.7	38	2	US-08-625-586-1	Sequence 1, Appli
29	193	45.7	38	3	US-09-128-401-1	Sequence 1, Appli
30	187	44.3	37	1	US-08-440-117-1	Sequence 1, Appli
31	187	44.3	37	4	US-09-068-738A-16	Sequence 16, Appli
32	186	44.1	38	5	PCT-US95-15800-29	Sequence 29, Appli
33	183	43.4	36	1	US-08-256-363-4	Sequence 4, Appli
34	179	42.4	34	1	US-08-256-363-2	Sequence 2, Appli
35	179	42.4	35	1	US-08-256-363-3	Sequence 3, Appli
36	179	42.4	36	1	US-08-112-024-2	Sequence 2, Appli
37	175	41.5	33	1	US-08-256-363-1	Sequence 1, Appli
38	175	41.5	34	1	US-07-763-373-1	Sequence 1, Appli
39	175	41.5	34	1	US-08-033-099-1	Sequence 1, Appli
40	175	41.5	34	1	US-08-262-495C-1	Sequence 1, Appli
41	175	41.5	34	1	US-07-915-247A-1	Sequence 1, Appli
42	175	41.5	34	1	US-08-443-863-1	Sequence 1, Appli
43	175	41.5	34	1	US-08-448-070-1	Sequence 1, Appli
44	175	41.5	34	1	US-08-488-105-7	Sequence 7, Appli
45	175	41.5	34	1	US-08-468-275-6	Sequence 6, Appli

## ALIGNMENTS

RESULT 1  
US-07-863-014-2  
: Sequence 2, Application US/07863014  
: Patent No. 5382658  
: GENERAL INFORMATION:  
: APPLICANT: KRONIS, K. Anne  
: APPLICANT: BOZZATO, Richard P.  
: TITLE OF INVENTION: STABILITY-ENHANCED VARIANTS OF  
: TITLE OF INVENTION: PARATHYROID HORMONE  
: NUMBER OF SEQUENCES: 8  
: CORRESPONDENCE ADDRESSES:  
: ADDRESSEE: Foley & Lardner  
: STREET: 1800 Diagonal Road, Suite 500  
: CITY: Alexandria  
: STATE: Virginia  
: COUNTRY: USA  
: ZIP: 22313-0299  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07/863,014  
: FILING DATE: 19920403  
: CLASSIFICATION: 530  
: ATTORNEY/AGENT INFORMATION:  
: NAME: BENT, Stephen A.  
: REGISTRATION NUMBER: 29,768  
: REFERENCE/DOCKET NUMBER: 16777/163 ALLE  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (703)836-9300  
: TELEFAX: (703)683-4109  
: TELEX: 899149  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 84 amino acids  
: TYPE: AMINO ACID  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-07-863-014-2

Query Match 98.8%, Score 417, DB 1, Length 84;  
Best Local Similarity 98.8%, Pred. No. 1.4e+44;  
Matches 82, Conservative 1, Mismatches 0, Indels 0, Gaps 0;  
OY 1 VSEIQLMNLGKHLNSMERVLRKKLDVHNFVALGAPLRDAGSORPRKKEDNVIVE 60  
DB 2 VSEIQLMNLGKHLNSMERVLRKKLDVHNFVALGAPLRDAGSORPRKKEDNVIVE 61



MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/835,231  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,709  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: 07/838,857  
FILING DATE: 18-FEB-1992  
APPLICATION NUMBER: JP 024841  
FILING DATE: 19-FEB-1991  
APPLICATION NUMBER: JP 0271438  
FILING DATE: 18-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: DAVID, RESNICK S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 41614-FWC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: 200291 STRE  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-835-231-9

Query Match 98.8%; Score 417; DB 2; Length 84;  
Best Local Similarity 98.8%; Pred. No. 1.4e-44;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSEIOLMHNIGKHLNLSMERVEWLRKKLDVHNHVALGAPLAPRDAGSQRPKKEDNVIVE 60  
Db 2 VSEIOLMHNIGKHLNLSMERVEWLRKKLDVHNHVALGAPLAPRDAGSQRPKKEDNVIVE 61

Qy 61 SHEKSLGEANKADVNVLTAKSQ 83  
Db 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 5  
US-08-805-918-3  
Sequence 3, Application US/08805918  
Patent No. 5885821  
GENERAL INFORMATION:  
APPLICANT: MAGOTA, Koji  
APPLICANT: MASUDA, Toyofumi  
APPLICANT: SUZUKI, Yuji  
APPLICANT: YABUTA, Masayuki  
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF SECRETORY KEX2  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/805,918  
FILING DATE: 04-MAR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-073217  
FILING DATE: 04-MAR-1996  
APPLICATION NUMBER: JP 8-352580  
FILING DATE: 16-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 001560-295  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-805-918-3

Query Match 98.8%; Score 417; DB 2; Length 84;  
Best Local Similarity 98.8%; Pred. No. 1.4e-44;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSEIOLMHNIGKHLNLSMERVEWLRKKLDVHNHVALGAPLAPRDAGSQRPKKEDNVIVE 60  
Db 2 VSEIOLMHNIGKHLNLSMERVEWLRKKLDVHNHVALGAPLAPRDAGSQRPKKEDNVIVE 61

Qy 61 SHEKSLGEANKADVNVLTAKSQ 83  
Db 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 6  
US-09-108-661-9  
Sequence 9, Application US/09108661  
Patent No. 6287806  
GENERAL INFORMATION:  
APPLICANT: NISHIMURA, Osamu  
APPLICANT: KURIYAMA, Masato  
APPLICANT: Koyama, No. 6287806uyuki  
APPLICANT: FUKUDA, Tsunebiko  
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY  
ACTIVE RECOMBINANT CYSTEINE-FREE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/108,661  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,709  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: 07/838,857

;; FILING DATE: 18-FEB-1992  
;; APPLICATION NUMBER: JP 024841  
;; FILING DATE: 19-FEB-1991  
;; APPLICATION NUMBER: JP 0271438  
;; FILING DATE: 18-OCT-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: DAVID, RESNICK S  
;; REGISTRATION NUMBER: 34,235  
;; REFERENCE/DOCKET NUMBER: 41614-FWC  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-523-3400  
;; TELEFAX: 617-523-6440  
;; TELEX: 200291 STRE  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 84 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHEICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: N-terminal  
;; ORIGINAL SOURCE:  
US-09-108-661-9

Query Match 98.8%; Score 417; DB 4; Length 84;  
Best local Similarity 98.8%; Pred. No. 1.4e-44;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMEREWLRRKLDVHNFVAGLAPLPADGSRPRKKEDNVLYE 60  
|||  
Db 2 VSEIQLMHNIGKHLNSMEREWLRRKLDVHNFVAGLAPLPADGSRPRKKEDNVLYE 61  
QY 61 SHEKSLGEADKADVNLTKAKSQ 83  
|||  
Db 62 SHEKSLGEADKADVNLTKAKSQ 84

## RESULT 7

PCT-US95-15800-25  
; Sequence 25, Application PC/TUS9515800  
; GENERAL INFORMATION:  
; APPLICANT: Bionebraska, Inc.  
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING  
; TITLE OF INVENTION: RECOMBINANT FUSION PROTEIN CONSTRUCTS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 Northwest Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/15800  
; FILING DATE: 07-DEC-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/350,530  
; FILING DATE: 07-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.45USMO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/332-5300  
; TELEFAX: 612/332-9081

;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 25:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 84 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHEICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: Internal  
;; ORIGINAL SOURCE:  
PCT-US95-15800-25

Query Match 98.8%; Score 417; DB 5; Length 84;  
Best local Similarity 98.8%; Pred. No. 1.4e-44;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMEREWLRRKLDVHNFVAGLAPLPADGSRPRKKEDNVLYE 60  
|||  
Db 2 VSEIQLMHNIGKHLNSMEREWLRRKLDVHNFVAGLAPLPADGSRPRKKEDNVLYE 61  
QY 61 SHEKSLGEADKADVNLTKAKSQ 83  
|||  
Db 62 SHEKSLGEADKADVNLTKAKSQ 84

## RESULT 8

US-08-142-551B-1  
; Sequence 1, Application US/08142551B  
; Patent No. 5814603  
; GENERAL INFORMATION:  
; APPLICANT: Oldenburg, Kevin R.  
; APPLICANT: Selick, Harold E.  
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND  
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: US  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/142,551B  
; FILING DATE: 25-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/077,296  
; FILING DATE: 14-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/898,219  
; FILING DATE: 12-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/965,677  
; FILING DATE: 22-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald F.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 854-7400  
; TELEFAX: (415) 854-8275  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 84 amino acids  
; TYPE: amino acid

TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..84  
OTHER INFORMATION: /note="84 amino acid PTH"  
US-08-142-551B-1

Query Match 97.6%; Score 412; DB 2; Length 84;  
Best Local Similarity 97.6%; Pred.No.5.9e-44;  
Matches 81; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIOLMHNIGKHLNLSMERVEWLRKKLDVHNHVALGAPLAPRDAGSQRP RKEDNVIVE 60  
|||||  
DB 2 VSEIOLMHNIGKHLNLSMERVEWLRKKLDVHNHVALGAPLAPRDAGSQRP RKEDNVIVE 61  
|||||  
QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
|||||  
DB 62 SHEKSLGEADKADVNVLTAKSQ 84

RESULT 9  
US-08-411-726-1  
; Sequence 1, Application US/08411726  
; Patent No. 5880093

GENERAL INFORMATION:

APPLICANT: BAGNOLI, Franco  
TITLE OF INVENTION: Use of Parathormone, Its Biologically  
TITLE OF INVENTION: Active Fragments and Correlated Peptides, for The Preparation  
TITLE OF INVENTION: Pharmaceutical Compositions Useful for The Treatment of Pregn  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenyon & Kenyon  
STREET: 1 Broadway  
CITY: New York  
STATE: NY  
COUNTRY: US  
ZIP: 10004

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2  
SOFTWARE: WordPerfect 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/411,726  
FILING DATE: 05-APR-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/02755

FILING DATE: 08-OCT-1993

APPLICATION NUMBER: MI-92A002331

FILING DATE: 09-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: PALMESE, Maria Luisa

REGISTRATION NUMBER: 34,402

REFERENCE/DOCKET NUMBER: 2111/1300

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-425-7200

TELEFAX: 212-425-5288

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-411-726-1

Query Match 97.6%; Score 412; DB 2; Length 84;  
Best Local Similarity 97.6%; Pred.No.5.9e-44;  
Matches 81; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIOLMHNIGKHLNLSMERVEWLRKKLDVHNHVALGAPLAPRDAGSQRP RKEDNVIVE 60

DB 2 VSEIOLMHNIGKHLNLSMERVEWLRKKLDVHNHVALGAPLAPRDAGSQRP RKEDNVIVE 61  
|||||

QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
|||||  
DB 62 SHEKSLGEADKADVNVLTAKSQ 84

RESULT 10

US-07-707-114-1

; Sequence 1, Application US/07707114

; Patent No. 5208041

GENERAL INFORMATION:

APPLICANT: SINDREY, Dennis R.

TITLE OF INVENTION: ESSENTIALLY PURE HUMAN PARATHYROID

TITLE OF INVENTION: HORMONE

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/707,114

FILING DATE: 19910523

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16777/147 ALLE

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: homo sapiens

IMMEDIATE SOURCE:

CLONE: hPTH

US-07-707-114-1

Query Match 96.4%; Score 407; DB 1; Length 84;  
Best Local Similarity 96.4%; Pred.No.2.5e-43;

Matches 80; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIOLMHNIGKHLNLSMERVEWLRKKLDVHNHVALGAPLAPRDAGSQRP RKEDNVIVE 60  
|||||  
DB 2 VSEIOLMHNIGKHLNLSMERVEWLRKKLDVHNHVALGAPLAPRDAGSQRP RKEDNVIVE 61  
|||||

QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
|||||  
DB 62 SHEKSLGEADKADVNVLTAKSQ 84

RESULT 11

US-07-773-098-2

; Sequence 2, Application US/07773098

; Patent No. 5317010

GENERAL INFORMATION:

APPLICANT: PANG, Peter K.T.

APPLICANT: JIE, Shan

;; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES AS  
;; TITLE OF INVENTION: OSTROPOROTIC CONTROL AGENTS  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Armstrong, Nikola, Marmelstein, Kubovcik &  
;; STREET: 1725 K Street, N.W., Suite 1000  
;; CITY: Washington D.C.  
;; COUNTRY: United States of America  
;; ZIP: 20006  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/773,098  
;; FILING DATE: 19911010  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Murray, Robert B.  
;; REGISTRATION NUMBER: 22,890  
;; REFERENCE/DOCKET NUMBER: 901930  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 659-2930  
;; TELEFAX: (202) 887-0357  
;; TELEEX: 440142  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 84 amino acids  
;; TYPE: AMINO ACID  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-07-773-098-2

Query Match 87.2%; Score 368; DB 1; Length 84;  
Best Local Similarity 88.0%; Pred. No. 1.7e-38;  
Matches 73; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSEREWLRKKLDVHNFAVGAPLPADAGSQRPRKKEDNVLE 60  
DB 2 VSEIQLMHNIGKHLNSEREWLRKKLDVHNFAVGASIAVYDGSORPRKKEDNVLE 61

QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
DB 62 SHEKSLGEADKADVDVLTAKAPQ 84

RESULT 12  
US-08-733-446-5  
; Sequence 5, Application US/08733446  
; Patent No. 5856138  
; GENERAL INFORMATION:  
; APPLICANT: FUKUDA, Tsunehiko  
; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MOTETINS AND  
; TITLE OF INVENTION: PRODUCTION THEREOF  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/773,446  
; FILING DATE: 18-OCT-1996

;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/402,970  
;; FILING DATE:  
;; APPLICATION NUMBER: US/07/926,787  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: NEUGER, George W  
;; REGISTRATION NUMBER: 26964  
;; REFERENCE/DOCKET NUMBER: 42025  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617)523-3400  
;; TELEFAX: (617)523-6440  
;; TELEEX: 200291 STRE UR  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 84 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FEATURE:  
;; NAME/KEY: mutation  
;; LOCATION: 8 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,  
;; LOCATION: 18 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,  
;; LOCATION: 34 Xaa=Cys or Phe, 35 Xaa=Cys or Val,  
;; LOCATION: 37 Xaa=Cys or Leu, 39 Xaa=Cys or Ala,  
;; LOCATION: 41 Xaa=Cys or Leu, 43 Xaa=Cys or Pro, 44 Xaa=Cys or Arg  
;; IDENTIFICATION METHOD: E  
;; US-08-733-446-5

Query Match 86.3%; Score 364; DB 2; Length 84;  
Best Local Similarity 88.0%; Pred. No. 5.3e-38;  
Matches 73; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSEREWLRKKLDVHNFAVGAPLPADAGSQRPRKKEDNVLE 60  
DB 2 VSEIQLMHNIGKHLNSEREWLRKKLDVHNXAXGXPAXXDAGSQRPRKKEDNVLE 61

QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
DB 62 SHEKSLGEADKADVDVLTAKSQ 84

RESULT 13  
US-07-773-098-1  
; Sequence 1, Application US/07773098  
; Patent No. 5317010  
; GENERAL INFORMATION:  
; APPLICANT: PANG, Peter K.T.  
; APPLICANT: JIE, Shan  
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES AS  
; TITLE OF INVENTION: OSTROPOROTIC CONTROL AGENTS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Armstrong, Nikola, Marmelstein, Kubovcik &  
; ADDRESSEE: Murray  
; STREET: 1725 K Street, N.W., Suite 1000  
; CITY: Washington D.C.  
; COUNTRY: United States of America  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/773,098  
; FILING DATE: 19911010  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murray, Robert B.  
; REGISTRATION NUMBER: 22,890  
; REFERENCE/DOCKET NUMBER: 901930



```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-773-098-1

Query Match
Best Local Similarity 85.1%; Score 359; DB 1; Length 84;
Matches 71; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNLSMERVEWMLRKRLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 60
DB 2 VSEIQFMHNLGKHLNLSMERVEWMLRKRLQDVHNFVALGASIVHRDGSQRPKKEDNVLYE 61

QY 61 SHEKSLGEADKADVNVLTAKSQ 83
DB 62 SHQKSLGEADKADVNVLTAKPQ 84

RESULT 14
US-08-733-446-4
; Sequence 4, Application US/08733446
; Patent No. 5856138
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTPINS AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,446
; FILING DATE: 18-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,970
; FILING DATE:
; APPLICATION NUMBER: US/07/926,787
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 42025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: mutation
; LOCATION: 5 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,
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; LOCATION: 15 Xaa=Leu, Ile, Val, Phe, Tyr, Trp or Met,
; LOCATION: 31 Xaa-Cys or Phe, 32 Xaa-Cys or Val,
; LOCATION: 34 Xaa-Cys or Leu, 36 Xaa-Cys or Ala,
; LOCATION: 38 Xaa-Cys or Leu, 40 Xaa-Cys or Pro, 41 Xaa-Cys or Arg
; IDENTIFICATION METHOD: E
; US-08-733-446-4

Query Match
Best Local Similarity 84.4%; Score 356; DB 2; Length 81;
Matches 71; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 EIQLMHNLGKHLNLSMERVEWMLRKRLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLYESH 62
DB 1 EIQLMHNLGKHLNLSMERVEWMLRKRLQDVHNFVALGASIXXGKXAXXDAGSQRPKKEDNVLYESH 60

QY 63 EKSLGEADKADVNVLTAKSQ 83
DB 61 EKSLGEADKADVNVLTAKSQ 81

RESULT 15
US-07-776-272-14
; Sequence 14, Application US/07776272
; Patent No. 5612454
; GENERAL INFORMATION:
; APPLICANT: Kaminuma, Toshihiko
; APPLICANT: Iida, Toshihiko
; APPLICANT: Tajima, Masahiro
; TITLE OF INVENTION: Process for Purification of Polypeptide
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player
; STREET: 1233 20th St. N.W. P.O. Box 18218
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: United States of America
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/776,272
; FILING DATE: 19911129
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-450-23167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-0400
; TELEFAX: 202-887-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Swine
; US-07-776-272-14

Query Match
Best Local Similarity 83.4%; Score 352; DB 1; Length 84;
Matches 69; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNLSMERVEWMLRKRLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 60
DB 2 VSEIQLMHNLGKHLNLSMERVEWMLRKRLQDVHNFVALGASIVHRDGSQRPKKEDNVLYE 61
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QY 61 SHEKSLGEANKADVNLTKAKSQ 83  
|:|||||:| |:|||||  
Db 62 SHOKSLGEADDKAAVDVLLIRAKPQ 84

Search completed: March 13, 2003, 14:52:54  
Job time : 15.2463 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2003, 14:58:49 ; Search time 16.1045 Seconds  
(without alignments)  
495.462 Million cell updates/sec

Title: US-09-636-530-2

Perfect score: 422

Sequence: 1 VSEIQLMHNIGKHLNSMERV.....KSLGEANKADVNLTKAKSQ 83

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR\_73:.\*  
2: PIR1:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417	98.8	115	1 PTHU	parathyroid hormone
2	366	86.7	115	2 JC4202	parathyroid hormone
3	359	85.1	115	1 PTHO	parathyroid hormone
4	355	84.1	115	1 PTHG	parathyroid hormone
5	311	73.7	115	2 A05091	parathyroid hormone
6	303	71.8	105	2 A1851	parathyroid hormone
7	174.5	41.4	119	2 A34937	parathyroid hormone
8	72.5	17.2	824	2 F72408	DNA polymerase III
9	72	17.1	1257	1 A58383	leucine-CRNA ligase
10	69.5	16.5	555	2 T44010	retinoblastoma bin
11	67.5	16.0	1156	2 B70356	virion protein lim
12	67.5	15.9	443	2 E82046	chromosome assembl
13	67	15.9	653	2 C71438	proteinase HsIV
14	67	15.9	674	2 B71438	hypothetical prote
15	66.5	15.8	378	2 F56653	hypothetical prote
16	66	15.6	215	2 T23195	virion protein - h
17	66	15.6	396	2 G96934	hypothetical prote
18	66	15.6	1163	2 F84669	DNA damage repair
19	66	15.6	19	2 H86803	probable chromosom
20	65	15.4	283	2 H86803	prophage p13 prote
21	65	15.4	1244	2 T23744	chromosome-associa
22	64.5	15.3	205	2 A86506	GMP kinase (import
23	64.5	15.3	205	2 F72117	guanylate kinase C
24	64.5	15.3	1018	2 T40253	hypothetical prote
25	64	15.2	166	2 T43497	hypothetical prote
26	64	15.2	642	2 D81401	probable flagellar
27	63.5	15.0	417	2 E70207	antigen S1 - Lyme
28	63.5	15.0	487	2 A71407	probable Ste20-like
29	63.5	15.0	797	2 A96232	succinoglycan bios

30	63.5	15.0	797	2 AD3054	hypothetical prote
31	63.5	15.0	1270	2 T09194	adaptor protein in
32	63	14.9	108	2 T37558	probable methyltra
33	63	14.9	672	2 T42186	conserved hypotnet
34	63	14.9	862	2 A05028	prote protein homol
35	63	14.9	992	2 A39531	protein-tyrosine k
36	63	14.9	1000	2 S18827	Flt3 protein - mou
37	63	14.9	1033	2 S73693	MG328 homolog P01
38	63	14.9	1937	2 T38055	myosin heavy chain
39	63	14.9	2109	2 T38414	transcription fact
40	63	14.9	5005	2 F82884	hypothetical prote
41	62.5	14.8	370	1 D64650	probable membrane
42	62.5	14.8	415	2 T34156	hypothetical prote
43	62.5	14.8	509	2 T29291	hypothetical prote
44	62.5	14.8	673	2 S54182	low affinity penic
45	62.5	14.8	674	2 S54178	low affinity penic

#### ALIGNMENTS

##### RESULT 1

PTHU

parathyroid hormone precursor [validated] - human  
N:Alternate names: proparathyroid hormone

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence\_revision 19-Jan-1996 #text\_change 08-Dec-2000

C:Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94410;

R:Vasick, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr.

Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983

A:Title: Nucleotide sequence of the human parathyroid hormone gene.

A:Reference number: A19339; MUID:83169834; PMID:6220408

A:Accession: A19339

A:Molecule type: DNA

A:Residues: 1-115 <VAS>

A:Cross-references: GB:J00301; NID:G190702; PIDN:AAA60215.1; PID:G190704

R:Yamauchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.

Biol. Chem. Hoppe-Seyler 375, 821-824, 1994

A:Title: Purification of meprin from human kidney and its role in parathyroid hormone

A:Reference number: S53790; MUID:95225986; PMID:7710697

A:Accession: S53790

A:Molecule type: protein

A:Residues: 'X',33,'X',35-46;65-84;105-110 <YAM>

A>Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occu

R:Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.

Nature 249, 155-157, 1974

A:Title: Structural analysis of human proparathyroid hormone by a new microsequencing

A:Reference number: A93169; MUID:74174967; PMID:4833516

A:Accession: A93169

A:Molecule type: protein

A:Residues: 26-37 <JAC>

R:Olstad, O.K.; Kreppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik,

Eur. J. Biochem. 205, 311-319, 1992

A:Title: Isolation and characterization of two biologically active O-glycosylated for

ation.

A:Reference number: S21199; MUID:92209518; PMID:1555591

A:Accession: S21199

A:Molecule type: protein

A:Residues: 32-114,'N' <OLS>

A>Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylati

R:Niell, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L

Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974

A:Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyro

A:Reference number: A93789; MUID:74111656; PMID:4521809

A:Accession: A93789

A:Molecule type: protein

A:Residues: 32-68 <NTA>

R:Brewer Jr., H.B.; Fairwell, T.; Roman, R.; Sizemore, G.W.; Arnaud, C.D.

Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

A:Title: Human parathyroid hormone; amino-acid sequence of the amino-terminal residue

A:Reference number: A93783; MUID:73070429; PMID:4509319

A:Accession: A93783

A:Molecule type: protein

A:Residues: 32-52, 'Q', 54-58, 'K', 60, 'L', 62-65 <BRE>  
 A:Note: this sequence was determined by sequenator and mass spectroscopic identification  
 A:Neumann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.  
 Biochemistry 14, 1842-1847, 1975  
 A:Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.  
 A:Reference number: A90387; PMID:75146516; PMID:1125201  
 A:Accession: A90387  
 A:Molecule type: protein  
 A:Residues: 52-75 <KE3>  
 A:Neumann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.  
 Biochemistry 17, 5723-5729, 1978  
 A:Title: Complete amino acid sequence of human parathyroid hormone.  
 A:Reference number: A90426; PMID:79082855; PMID:728431  
 A:Accession: A90426  
 A:Molecule type: protein  
 A:Residues: 61-106, 'D', 108-115 <KEU>  
 A:Neumann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.  
 In Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-  
 A:Reference number: A94410  
 A:Accession: A94410  
 A:Molecule type: protein  
 A:Residues: 75-100 <KE2>  
 R:Regear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J.  
 Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974  
 A:Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of hum  
 A:Reference number: A91660; PMID:75059220; PMID:4474131  
 A:Contents: annotation; synthesis of residues 32-65  
 A:Note: the biologically active amino-terminal 34 residues of parathyroid hormone were s  
 at renal adenylyl cyclase assay and with the bovine hormone's active region in the chid  
 R:Andeatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Rinkler, B.; Rittel,  
 Helv. Chim. Acta 56, 470-473, 1973  
 A:Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.  
 A:Reference number: A91635; PMID:73227467; PMID:4721748  
 A:Contents: annotation; synthesis of residues 32-65  
 A:Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined  
 into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level  
 R:Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981  
 A:Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.  
 A:Reference number: I38342; PMID:82150870; PMID:6950381  
 A:Accession: I38342  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-115 <RES>  
 A:Cross-references: EMBL:V00597; NID:937143; PIDN:CAA23843.1; PID:937144  
 C:Genetics:  
 A:Gene: GDB:PTH  
 A:Cross-references: GDB:119522; OMIM:168450  
 A:Map position: 11p15.2-11p15.1  
 A:Introns: 29/2  
 A:Note: the first intron occurs before the initiator codon  
 C:Function:  
 A:Description: factor in homeostatic control of plasma calcium and phosphate; released b  
 counter to calctonin  
 C:Superfamily: parathyroid hormone; parathyroid hormone homology  
 C:Keywords: calcium; hormone; parathyroid gland; plasma  
 F.1-23/Domain: signal sequence #status predicted <SIG>  
 F.26-31/Domain: propeptide #status experimental <ROS>  
 F.30-64/Domain: parathyroid hormone homology <PTH>  
 F.32-115/Product: parathyroid hormone #status experimental <MAT>  
 Query Match 98.8%; Score 417; DB 1; Length 115;  
 Best Local Similarity 98.8%; Pred. No. 5, 1e-37;  
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VSEIQLMHNIGKHLNSMEREWLRRKLDQVHNFVALGAPLAPDAGSQRRKKEDNVLYE 60  
 DB 33 VSEIQFMHNIGKHLNSMEREWLRRKLDQVHNFVALGAPLAPDAGSQRRKKEDNVLYE 92  
 OY 61 SHEKSLGEANKADVNVLTAKSQ 83  
 DB 93 SHEKSLGEADKADVNVLTAKSQ 115

RESULT 2  
 JC4202  
 parathyroid hormone precursor - dog  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 16-Jul-1999  
 C:Accession: JC4202  
 R:Rosol, T.J.; Steilmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.  
 Gene 160, 241-243, 1995  
 A:Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein a  
 A:Reference number: JC4201; PMID:95369696; PMID:7642102  
 A:Accession: JC4202  
 A:Molecule type: mRNA  
 A:Residues: 1-115 <ROS>  
 A:Cross-references: GB:U15662; NID:9558915; PIDN:AAA82584.1; PID:9558916  
 C:Superfamily: parathyroid hormone; parathyroid hormone homology  
 C:Keywords: hormone  
 F.1-31/Domain: signal sequence #status predicted <SIG>  
 F.30-64/Domain: parathyroid hormone homology <PTH>  
 F.32-115/Product: parathyroid hormone #status predicted <MAT>

Query Match 86.7%; Score 366; DB 2; Length 115;  
 Best Local Similarity 86.7%; Pred. No. 1, 3e-31;  
 Matches 72; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMEREWLRRKLDQVHNFVALGAPLAPDAGSQRRKKEDNVLYE 60  
 DB 33 VSEIQFMHNIGKHLNSMEREWLRRKLDQVHNFVALGAPLAPDAGSQRRKKEDNVLYE 92  
 OY 61 SHEKSLGEANKADVNVLTAKSQ 83  
 DB 93 SHEKSLGEADKADVNVLTAKSQ 115

RESULT 3  
 PTHO  
 parathyroid hormone precursor - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 18-Jun-1999  
 C:Accession: A24949; A93835; A91648; A93773; I45975; I45976; A01534  
 R:Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.  
 Gene 28, 319-329, 1984  
 A:Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroi  
 A:Reference number: A24949; PMID:84262483; PMID:6086460  
 A:Accession: A24949  
 A:Molecule type: DNA  
 A:Residues: 1-115 <WEA>  
 A:Cross-references: GB:K01938  
 R:Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr  
 Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979  
 A:Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid h  
 A:Reference number: A93835; PMID:80056617; PMID:388425  
 A:Accession: A93835  
 A:Molecule type: DNA  
 A:Residues: 1-115 <KRO>  
 A:Cross-references: GB:V00106; GB:J00023; NID:984; PIDN:CAA23439.1; PID:985  
 A:Note: the authors translated the codon GAA for residue 50 as Gly  
 R:Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D  
 Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974  
 A:Title: The N-terminal amino acid sequence of bovine preproparathyroid hormone.  
 A:Reference number: A93793; PMID:74142666; PMID:4522780  
 A:Accession: A93793  
 A:Molecule type: protein  
 A:Residues: 26-115 <HAM>  
 R:Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; P  
 Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970  
 A:Title: The amino acid sequence of bovine parathyroid hormone I.  
 A:Reference number: A91648; PMID:71076162; PMID:5531031  
 A:Accession: A91648  
 A:Molecule type: protein  
 A:Residues: 32-115 <NIA>  
 R:Brewer Jr., H.B.; Roman, R.  
 Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970

A:Title: Bovine parathyroid hormone: amino acid sequence.  
A:Reference number: A93773; MUID:71063634; PMID:5275384  
A:Accession: A93773  
A:Molecule type: protein  
A:Residues: 32-115 <BHE>  
R:Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Mall, H.D.; Sauer, R.; Deflos, L.J.;  
Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971  
A:Title: Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyroid hormone.  
A:Reference number: A93776; MUID:71091588; PMID:4322265  
A:Contents: annotation; synthesis of residues 32-65  
A:Note: the synthetic peptide was active in vivo and in vitro  
R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.  
Am. J. Med. 56, 759-766, 1974  
A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone.  
A:Reference number: A90030; MUID:74173303; PMID:4598526  
A:Contents: annotation  
R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.  
Am. J. Med. 56, 759-766, 1974  
A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone.  
A:Reference number: A90030; MUID:74173303; PMID:4598526  
A:Contents: annotation  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: calcium; hormone; parathyroid gland  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-31/Domain: propeptide #status experimental <PRO>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status experimental <MAT>  
Mol. Cell. Endocrinol. 28, 411-424, 1982  
A:Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.  
A:Reference number: 145976; MUID:8105964; PMID:6185374  
A:Accession: 145976  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <ME2>  
A:Cross-references: GB:U00024; NID:g163642; PIDN:AAA30747.1; PID:g163643  
R:Meaver, C.A.; Gordon, D.F.  
Mol. Cell. Endocrinol. 28, 411-424, 1982  
A:Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.  
A:Reference number: 145976; MUID:8105964; PMID:6185374  
A:Accession: 145976  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <ME3>  
A:Cross-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645  
C:Genetics:  
A:Gene: PTH  
A:Introns: 29/2  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: hormone  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-31/Domain: propeptide #status experimental <PRO>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status experimental <MAT>  
Query Match 85.1%; Score 359; DB 1; Length 115;  
Best Local Similarity 85.3%; Pred. No. 6.9e-31;  
Matches 71; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
Oy 1 VSEIOLMNLGKHLNSMRVEMLRKKLDDVHNFFVALGAPLAPRDAGSORPRKKEDNVAVE 60  
Db 33 VSEIOLMNLGKHLNSMRVEMLRKKLDDVHNFFVALGASIVHRDGSORPRKKEDNVAVE 92  
Oy 61 SHEKSLGEANKRADVNVITKRSQ 83  
Db 93 SHOKSLGEADKADVDVLIKAKPQ 115  
RESULT 4  
PTPG  
parathyroid hormone precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 24-Apr-1984 #sequence.revision 12-Apr-1996 #text.change 18-Jun-1999  
R:Schmelzter, H.J.; Gross, G.; Widera, G.; Mayer, H.  
Nucleic Acids Res. 15, 6740, 1987  
A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone.  
A:Reference number: A26806; MUID:87316938; PMID:3628009  
A:Accession: B26806  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-115 <SCH>  
A:Cross-references: GB:X05722; GB:Y00409; NID:g1838; PIDN:CAA29193.1; PID:g1839

R:Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.  
Biochemistry 14, 3631-3635, 1975  
A:Title: Porcine preparathyroid hormone. Identification, biosynthesis, and partial amino acid sequence.  
A:Reference number: A90390; MUID:76018954; PMID:1164500  
A:Accession: A90390  
A:Molecule type: protein  
A:Residues: 26-115 <CHU>  
R:Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr.  
Biochemistry 13, 1994-1999, 1974  
A:Title: The amino acid sequence of porcine parathyroid hormone.  
A:Reference number: A90376; MUID:7425317; PMID:4840833  
A:Accession: A90376  
A:Molecule type: protein  
A:Residues: 32-109 <SAU>  
R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.  
Am. J. Med. 56, 759-766, 1974  
A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone.  
A:Reference number: A90030; MUID:74173303; PMID:4598526  
A:Contents: annotation  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: calcium; hormone; parathyroid gland  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-31/Domain: propeptide #status experimental <PRO>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status experimental <MAT>  
Query Match 84.1%; Score 355; DB 1; Length 115;  
Best Local Similarity 84.3%; Pred. No. 1.8e-30;  
Matches 70; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
Oy 1 VSEIOLMNLGKHLNSMRVEMLRKKLDDVHNFFVALGAPLAPRDAGSORPRKKEDNVAVE 60  
Db 33 VSEIOLMNLGKHLNSLTERVELRKKLDDVHNFFVALGASIVHRDGSORPRKKEDNVAVE 92  
Oy 61 SHEKSLGEANKRADVNVITKRSQ 83  
Db 93 SHOKSLGEADKADVDVLIKAKPQ 115  
RESULT 5  
PTPG  
parathyroid hormone precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 05-Jun-1987 #sequence.revision 05-Jun-1987 #text.change 16-Jul-1999  
R:Heinrich, G.; Kromenbery, H.M.; Potts Jr., J.T.; Habener, J.F.  
J. Biol. Chem. 259, 3320-3329, 1984  
A:Reference number: A05091; MUID:84135846; PMID:6321505  
A:Accession: A05091  
A:Molecule type: DNA  
A:Residues: 1-115 <HEI>  
A:Cross-references: GB:K01268; NID:g206483; PIDN:AAA41979.1; PID:g206485  
A:Note: the authors translated the codon GAA for residue 87 as Asp  
R:Schmelzter, H.J.; Gross, G.; Widera, G.; Mayer, H.  
Nucleic Acids Res. 15, 6740, 1987  
A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone.  
A:Reference number: A26806; MUID:87316938; PMID:3628009  
A:Accession: A26806  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-115 <SCH>  
A:Cross-references: GB:X05721; GB:Y00409; NID:g556002; PIDN:CAA29192.1; PID:g556003  
C:Genetics:  
A:Introns: 29/3  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
F:30-64/Domain: parathyroid hormone homology <PTH>  
Query Match 73.7%; Score 311; DB 2; Length 115;  
Best Local Similarity 72.3%; Pred. No. 8.2e-26;  
Matches 160; Conservative 11; Mismatches 12; Indels 0; Gaps 0;  
Oy 1 VSEIOLMNLGKHLNSMRVEMLRKKLDDVHNFFVALGAPLAPRDAGSORPRKKEDNVAVE 60  
Db 33 VSEIOLMNLGKHLNSLTERVELRKKLDDVHNFFVALGASIVHRDGSORPRKKEDNVAVE 92



Db 692 MELVNLHLSOYLNSVPEENRRLRLREIVEKTLALSPFAPHLAEFEWHDLGN-----D 744  
 QY 56 NVLVE-----SHEKSLGEANKADVNLTKAK 81  
 Db 745 SLVVOOSMPSTYDPKALVEVEVEIAIDINCK 774

RESULT 10  
 158383  
 retinoblastoma binding protein 1, splice form I - human  
 N:Alternate names: retinoblastoma-associated protein 2 (misonmer)  
 M:Contains: retinoblastoma binding protein 1, splice form II  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
 C:Accession: 158383; 158390; 178883; S16953; B42997  
 R:Fatiaev, A.R.; Helin, K.; Dembski, M.S.; Dyson, N.; Harlow, E.; Vuocolo, G.A.; Hanobik  
 Oncogene 8, 3149-3156, 1993  
 A:Title: Characterization of the retinoblastoma binding proteins RBP1 and RBP2.  
 A:Reference number: 158383; MUID:94020841; PMID:8414517  
 A:Accession: 158383  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1257 <EAT>  
 A:Cross-references: GB:S66427; NID:9435775; PIDN:AA028543.1; PID:9435776  
 R:Olterson, G.A.; Kratzke, R.A.; Lin, A.Y.; Johnston, P.G.; Kaye, F.J.  
 Oncogene 8, 949-957, 1993  
 A:Title: Alternative splicing of the RBP1 gene clusters in an internal exon that encodes  
 A:Reference number: 158390; MUID:93205410; PMID:8455946  
 A:Accession: 158390  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 338-384, 'V', 386-617, 'R', 619-652, 'V', 654-778, 'T', 780-1257 <OTT1>  
 A:Cross-references: GB:S57153; NID:9298681; PIDN:AA025833.1; PID:9298682  
 A:Accession: 178883  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 338-384, 'V', 386-617, 'R', 619-652, 'V', 654-778, 'T', 780-1120, 1175-1257 <OTT2>  
 A:Cross-references: GB:S57160; NID:9298683; PIDN:AA025834.1; PID:9298684  
 R:Deleo-Jones, D.; Huang, P.S.; Jones, R.E.; Haskell, K.M.; Vuocolo, G.A.; Hanobik, M.G.  
 Nature 352, 251-254, 1991  
 A:Title: Cloning of cDNAs for cellular proteins that bind to the retinoblastoma gene pro  
 A:Reference number: S16953; MUID:91312450; PMID:1857421  
 A:Accession: S16953  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 855-1177, 'S', 1179-1195, 'SENITCL' <DCE>  
 R:Kaelin Jr., W.G.; Krek, W.; Sellers, W.R.; Decaprio, J.A.; Ajchenbaum, F.; Fuchs, C.S.  
 Cell 70, 351-364, 1992  
 A:Title: Expression cloning of a cDNA encoding a retinoblastoma-binding protein with E2F  
 A:Reference number: A42997; MUID:92346721; PMID:1638635  
 A:Accession: B42997  
 A:Molecule type: mRNA  
 A:Residues: 510-617, 'R', 619-1257 <KAE>  
 A:Experimental source: Akata cells  
 A:Note: the cited Genbank accession number, M96577, is apparently a misprint and does no  
 A:Gene: GDB:RBPI  
 A:Cross-references: GDB:120340; OMIM:180260  
 A:Map position: 3q21-3q22  
 C:Superfamily: human retinoblastoma binding protein 1  
 C:Keywords: alternative splicing  
 F:1-1257/Product: retinoblastoma binding protein 1, splice form II #status pre  
 F:1-1120, 1175-1257/Product: retinoblastoma binding protein 1, splice form I #status predicted <SF1

Query Match 17.1%; Score 72; DB 1; Length 1257;  
 Best Local Similarity 26.8%; Pred. No. 23;  
 Matches 19; Conservative 21; Mismatches 27; Indels 4; Gaps 2;

OY 13 HUNSEREYWLKKKODVHN-FVAGAPLAPRDAGSORPKKEDNVIVSHKSLGEANK 71  
 Db 1179 NNNSTERISFLOEKLOETIRKKYMSLKSEVATIDRRRRRLKKRDREV--SHAGASMSAS 1235

QY 72 ADVNLVLTAKS 82  
 Db 1236 SDTGMSPSSSS 1246

RESULT 11  
 744010  
 virion protein [imported] - human herpesvirus 6  
 C:Species: human herpesvirus 6  
 C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T44010; T44197  
 R:Risegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; K  
 J. Virol. 73, 8053-8063, 1999  
 A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A a  
 A:Reference number: 222732; MUID:99412319; PMID:10482554  
 A:Accession: T44010  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-555 <ISE>  
 A:Cross-references: EMBL:AB021506; NID:9495977; PIDN:BA078271.1; PID:949596038  
 A:Experimental source: strain HST; pop. variant B  
 R:Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Demhurst, S.; Inoue, N.; Pellett, P.E.  
 J. Virol. 73, 8040-8052, 1999  
 A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with hum  
 A:Reference number: 222734; MUID:99412318; PMID:10482553  
 A:Accession: T44197  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-555 <DOM>  
 A:Cross-references: EMBL:AF157706; PIDN:AA06348.1  
 A:Experimental source: strain 229; variant B  
 C:Genetics:  
 A:Gene: 050  
 C:Superfamily: varicella-zoster virus gene 34 protein

Query Match 16.5%; Score 69.5; DB 2; Length 555;  
 Best Local Similarity 35.4%; Pred. No. 16;  
 Matches 23; Conservative 10; Mismatches 27; Indels 5; Gaps 2;

QY 23 LKKKIDVNFVALGAPLAPRDAGSORPKKEDNVIVSHKSLGEA---NKADYNVLT 78  
 Db 42 LREKIDGHRDLRLRRLKTELDALQKMKQSDVL-NSHLKAIEDALLFTDGEVNET 100  
 QY 79 KAKSQ 83  
 Db 101 KADTQ 105

RESULT 12  
 B70356  
 chromosome assembly protein homolog - Aquifex aeolicus  
 C:Species: Aquifex aeolicus  
 C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 02-Jun-2000  
 C:Accession: B70356  
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;  
 V. Nature 392, 353-358, 1998  
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A:Reference number: A70300; MUID:98196666; PMID:9537320  
 A:Accession: B70356  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1156 <AGP>  
 A:Cross-references: GB:AE000699; NID:92983238; PIDN:AA06839.1; PID:92983243; GB:AE00  
 A:Experimental source: strain VFS  
 C:Genetics:  
 A:Gene: xcpC  
 C:Superfamily: chromosome segregation protein SWC1

Query Match 16.0%; Score 67.5; DB 2; Length 1156;  
 Best Local Similarity 29.0%; Pred. No. 61;  
 Matches 27; Conservative 16; Mismatches 25; Indels 25; Gaps 4;





GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: March 13, 2003, 14:52:59 ; Search time 9.29105 Seconds  
(without alignments)

370.522 Million cell updates/sec

Title: US-09-636-530-2  
Perfect score: 422  
Sequence: 1 VSEIQMLNGLKHLNSMERY.....KSLGEANKADVNLTKAKSQ 83

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417	98.8	115	1 PTHY_HUMAN	P01270 homo sapien
2	410	97.2	115	1 PTH_MACFA	G9xt33 macaca fasc
3	366	86.7	115	1 PTHY_CANFA	P52212 canis famlil
4	359	85.1	115	1 PTHY_BOVIN	P01268 bos taurus
5	355	84.1	115	1 PTHY_PIG	P01269 sus scrofa
6	311	73.7	115	1 PTHY_RAT	P04088 rattus norv
7	174.5	41.4	119	1 PTHY_CHICK	P15743 gallus gall
8	72.5	17.2	824	1 SYL_THENA	G9wy15 thermotoga
9	72	17.1	1257	1 RBB1_HUMAN	P29374 homo sapien
10	69.5	16.5	555	1 UL25_HSV62	P52537 human herpe
11	67	15.9	443	1 HSLU_VIRCH	G9kn27 vibrio chol
12	66.5	15.8	378	1 UL25_HSV66	P52536 human herpe
13	66.5	15.8	555	1 UL25_HSV60	P52387 human herpe
14	65	15.4	1244	1 MIX1_CAEBL	Q09591 caenorhabdi
15	64.5	15.3	205	1 KGU4_CHLPPN	Q92961 chlamydia p
16	64	15.2	642	1 FLID_CAMJE	G9phw6 campylobact
17	63.5	15.0	1270	1 ITN1_XENLA	Q42287 xenopus lae
18	63	14.9	992	1 ELT3_MOUSE	Q00342 mus musculu
19	63	14.9	1033	1 T328_MICEP	P75310 mycoplasma
20	63	14.9	1388	1 RPOD_TOBAC	P38550 nicotiana t
21	63	14.9	1937	1 MYH8_HUMAN	P13533 homo sapien
22	62.5	14.8	370	1 Y444_HELPY	Q25685 helicobacte
23	62.5	14.8	632	1 DNAK_ACTAC	G92046 mus musculu
24	62.5	14.8	1658	1 ITN2_MOUSE	P77746 escherichia
25	62	14.7	300	1 YBDO_ECOLI	O60231 homo sapien
26	62	14.7	1041	1 DD16_HUMAN	P18947 caenorhabdi
27	61.5	14.6	282	1 VIT4_CAEBL	P4180 haemophilus
28	61.5	14.6	366	1 YE05_HABIN	G9195 oryza sativ
29	61	14.5	429	1 DPD2_ORYSA	P53119 saccharomyc
30	61	14.5	910	1 HUL5_YEAST	Q16512 homo sapien
31	60.5	14.3	942	1 PKL1_HUMAN	Q15811 homo sapien
32	60.5	14.3	1721	1 ITN1_PSESS	P06618 pseudomonas
33	60	14.2	455	1 HYIN_PSESS	

34	60	14.2	668	1 DCRA_DESVH	P35841 desulfovibr
35	60	14.2	1027	1 KINN_MOUSE	P33175 mus musculu
36	60	14.2	1032	1 KINN_HUMAN	Q12840 homo sapien
37	60	14.2	1084	1 MYSS_RABIT	P02562 oryctolagus
38	60	14.2	1172	1 SYK2_MYCTU	P94974 mycobacteri
39	60	14.2	1935	1 MYSS_CYPBA	Q90339 cyprinus ca
40	60	14.2	1938	1 MYH4_RABIT	Q28641 oryctolagus
41	60	14.2	1940	1 MYH3_CHICK	P02565 gallus gall
42	60	14.2	2390	1 SPCC_HUMAN	O15020 homo sapien
43	59.5	14.1	437	1 MURC_STANU	O31211 straphylococ
44	59.5	14.1	1154	1 KDGD_MESAU	O64398 mesocricetu
45	59	14.0	177	1 PTHR_HUMAN	P12272 homo sapien

## ALIGNMENTS

RESULT 1	PTHY_HUMAN	STANDARD:	PRT:	115 AA.
ID	PTHY_HUMAN			
AC	P01270:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).			
GN	PTH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=82150870; PubMed=6950381;			
RA	Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;			
RT	"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid			
RL	hormone.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=83169834; PubMed=6220408;			
RA	Vasicek T.J., McDevitt B.E., Freeman M.W., Pennick B.J.,			
RA	Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;			
RT	"Nucleotide sequence of the human parathyroid hormone gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).			
RN	[3]			
RP	SEQUENCE OF 26-37.			
EX	MEDLINE=74174967; PubMed=4833516;			
RA	Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;			
RT	"Structural analysis of human parathyroid hormone by a new			
RL	microsequencing approach.";			
RL	Nature 249:155-157(1974).			
RN	[4]			
RP	SEQUENCE OF 32-68.			
EX	MEDLINE=74111656; PubMed=4521809;			
RA	Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,			
RA	O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;			
RT	"The amino-acid sequence of the amino-terminal 37 residues of human			
RL	parathyroid hormone.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).			
RN	[5]			
RP	SEQUENCE OF 61-83 AND 84-115.			
EX	MEDLINE=79082855; PubMed=728431;			
RA	Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,			
RT	Potts J.T. Jr.;			
RL	"Complete amino acid sequence of human parathyroid hormone.";			
RL	Biochemistry 17:5723-5729(1978).			
RN	[6]			
RP	SEQUENCE OF 75-100.			
EX	Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,			
RA	O'Riordan J.L.H., Potts J.T. Jr.;			
RA	(in) Talmadge R.V., Owen M., Parsons J.A. (eds.);			
RL	Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,			
RL	Amsterdam (1975).			

RN [7]  
 RP REVISIONS.  
 RX MEDLINE=75146516; PubMed=1125201;  
 RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;  
 RT "A reinvestigation of the amino-terminal sequence of human  
 RL parathyroid hormone.";  
 RN Biochemistry 14:1842-1847(1975).  
 (8)  
 RP SYNTHESIS OF 32-65.  
 RX MEDLINE=75059220; PubMed=4474131;  
 RA Tregear G.W., van Rietschoten J., Green E., Niall H.D.,  
 RT Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;  
 RL Solid-phase synthesis of the biologically active N-terminal 1-34  
 peptide of human parathyroid hormone.";  
 RN Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).  
 (9)  
 RP SYNTHESIS OF 32-65.  
 RX MEDLINE=73227467; PubMed=4721748;  
 RA Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,  
 RL Rinkler B., Rittel W., Sieber P.;  
 RN "Synthesis of sequence 1-34 of human parathyroid hormone.";  
 RL Helv. Chim. Acta 56:470-473(1973).  
 (10)  
 RP STRUCTURE BY NMR OF 32-65.  
 RX MEDLINE=91299748; PubMed=2069952;  
 RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;  
 RT "Investigation of the solution structure of the human parathyroid  
 RL hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry,  
 RT and molecular dynamics calculations.";  
 RL Biochemistry 30:6936-6942(1991).  
 (11)  
 RP STRUCTURE BY NMR OF 32-65.  
 RX MEDLINE=93345518; PubMed=8344299;  
 RA Barden J.A., Culbertson R.M.;  
 RT "Stabilized NMR structure of human parathyroid hormone(1-34).";  
 RL Eur. J. Biochem. 215:315-321(1993).  
 (12)  
 RP STRUCTURE BY NMR OF 32-68.  
 RX MEDLINE=95318084; PubMed=797503;  
 RA Marx U.C., Austermann S., Bayer P., Adermann K., Eljhart A.,  
 RA Sticht H., Walter S., Schmid F.-X., Jelenke R., Forssmann W.-G.,  
 RA Roesch P.;  
 RT "Structure of human parathyroid hormone 1-37 in solution.";  
 RL J. Biol. Chem. 270:15194-15202(1995).  
 (13)  
 RP STRUCTURE BY NMR OF 32-70.  
 RX MEDLINE=20090619; PubMed=10623601;  
 RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;  
 RT "Solution structures of human parathyroid hormone fragments  
 hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment  
 bPTH(1-37).";  
 RL Biochem. Biophys. Res. Commun. 267:213-220(2000).  
 (14)  
 RP VARIANT ARG-18.  
 RX MEDLINE=91009811; PubMed=2212001;  
 RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,  
 RA Kronenberg H.M.;  
 RT "Mutation of the signal peptide-encoding region of the  
 RL preproparathyroid hormone gene in familial isolated  
 RT hypoparathyroidism.";  
 RL J. Clin. Invest. 86:1084-1087(1990).  
 (15)  
 RP FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
 CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED  
 CC HYPOPARATHYROIDISM (FIH).  
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
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 CC -----  
 DR EMBL: J00301; AA60215.1; -;  
 DR EMBL: V00597; CA23843.1; -;  
 DR EMBL: A29146; CA01956.1; -;  
 DR PIR: A01536; PTHU.  
 DR PIR: A19339; A19339.  
 DR PDB: 1HPH; 10-JUL-95.  
 DR PDB: 1HTR; 15-OCT-97.  
 DR PDB: 1ZMA; 12-MAR-97.  
 DR PDB: 1ZMB; 12-MAR-97.  
 DR PDB: 1ZWD; 12-MAR-97.  
 DR PDB: 1ZWE; 12-MAR-97.  
 DR PDB: 1ZWF; 16-JUN-97.  
 DR PDB: 1ZWG; 16-JUN-97.  
 DR PDB: 1BMX; 14-JAN-00.  
 DR PDB: 1HPY; 14-JAN-00.  
 DR Genew; HGNC:9606; PTH.  
 DR MIM: 146200; -;  
 DR MIM: 168450; -;  
 DR InterPro: IPR001415; Parathyroid\_hrm.  
 DR InterPro: IPR003625; Pthyroid\_hrm\_sub.  
 DR Pfam: PF01279; Parathyroid; 1.  
 DR ProDom: PD010687; Pthyroid; 1.  
 DR SMART: SM00087; PTH; 1.  
 DR PROSITE: PS00335; PARATHYROID; 1.  
 KW Hormone; Signal; Disease mutation; 3D-structure.  
 FT SIGNAL 1 25  
 FT PROPEP 1 31  
 FT CHAIN 32 115  
 FT VARIANT 18 18  
 FT PARATHYROID HORMONE.  
 FT C -> R (IN FIH; LEADS TO INEFFICIENT  
 FT PROCESSING OF THE PRECURSOR).  
 FT /FTID-VAR 006047.  
 FT N -> D (IN REF. 5).  
 SQ SEQUENCE 115 AA; 12861 MW; 849015736A6E5597 CRC64;  
 Query Match 98.8%; Score 417; DB 1; Length 115;  
 Best Local Similarity 98.8%; Pred. No. 1.8e-39;  
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VSEIQIMHNIGKILNEMERWIKRKLQDVNHNVALCAPLPADASQRPKKEDNVLVE 60  
 DB 33 VSEIQIMHNIGKILNEMERWIKRKLQDVNHNVALCAPLPADASQRPKKEDNVLVE 92  
 QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
 DB 93 SHEKSLGEADKADVNVLTAKSQ 115  
 RESULT 2  
 PTH\_MACFA  
 ID PTH\_MACFA STANDARD: PRT: 115 AA.  
 AC 09XTJ35;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Parathyroid hormone precursor (Parathyrim) (PTH).  
 GN PTH.  
 OS Macaca fascicularis (Crah eating macaque) (synomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OC NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Malaiyilind S., Takenaka O.;  
 RT "Nucleotide sequences of parathyroid gene in five species of macaque  
 RL of Thailand.";  
 RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).  
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
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DR EMBL: AF130257; AAD42777.1; -.  
DR HSSP: P01270; IHPY.  
DR InterPro: IPR001415; Parathyroid\_hrm.  
DR InterPro: IPR003625; Pthyrhorm\_sub.  
DR Pfam: PF01279; Parathyroid; 1.  
DR ProDom: PD010687; Pthyrhorm\_sub; 1.  
DR SMART: SM00087; PTH; 1.  
DR PROSITE: PS00335; PARATHYROID; 1.  
KW Hormone; Signal.  
FT PROPEP 1 25 BY SIMILARITY.  
FT CHAIN 26 31 BY SIMILARITY.  
FT CHAIN 32 115 PARATHYROID HORMONE.  
SQ SEQUENCE 115 AA: 12890 MW: 8C2500EF24BE597 CRC64:

Query Match 97.2%; Score 410; DB 1; Length 115;  
Best Local Similarity 95.2%; Pred. No. 1.1e-38;  
Matches 79; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIOLMNLGKHLNLSMEVEWLRKKLDVHNHFGALAPLAPRDGSGRPKRKEDNVLE 60  
DB 33 VSEIOLMNLGKHLNLSMEVEWLRKKLDVHNHFGALAPLAPRDGSGRPKRKEDNVLE 92  
QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
DB 93 SHEKSLGEANKADVNVLTAKSQ 115

## RESULT 3

PTHY\_CANFA

ID PTHY\_CANFA STANDARD; PRT; 115 AA.

AC P52212;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Parathyroid hormone precursor (Parathyrin) (PTH).  
GN PTH.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Parathyroid;

RX MEDLINE=95369696; PubMed=7642102;

RA Rosol T.J., Steimeyer C.L., McCauley L.K., Groene A.,

RA Dewille J.W., Capen C.C.;

RT "Sequences of the cDNAs encoding canine parathyroid hormone-related  
protein and parathyroid hormone.";

RL Gene 160:241-243(1995).

RT Gene 160:241-243(1995).

RT -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
BONE AND PREVENTING THEIR RENAL EXCRETION.

RT -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: U15662; AA82584.1; -.  
DR HSSP: P01268; IZWC.  
DR InterPro: IPR001415; Parathyroid\_hrm.  
DR InterPro: IPR003625; Pthyrhorm\_sub.

DR Pfam: PF01279; Parathyroid; 1.  
DR ProDom: PD010687; Pthyrhorm\_sub; 1.  
DR SMART: SM00087; PTH; 1.  
DR PROSITE: PS00335; PARATHYROID; 1.  
KW Hormone; Signal.  
FT PROPEP 1 25 BY SIMILARITY.  
FT CHAIN 26 31 BY SIMILARITY.  
FT CHAIN 32 115 PARATHYROID HORMONE.  
SQ SEQUENCE 115 AA: 12957 MW: FC38F77F1C8CFE56 CRC64:

Query Match 86.7%; Score 366; DB 1; Length 115;  
Best Local Similarity 86.7%; Pred. No. 8.1e-34;  
Matches 72; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 VSEIOLMNLGKHLNLSMEVEWLRKKLDVHNHFGALAPLAPRDGSGRPKRKEDNVLE 60  
DB 33 VSEIOLMNLGKHLNLSMEVEWLRKKLDVHNHFGALAPLAPRDGSGRPKRKEDNVLE 92  
QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
DB 93 SHEKSLGEANKADVNVLTAKSQ 115

## RESULT 4

PTHY\_BOVIN

ID PTHY\_BOVIN STANDARD; PRT; 115 AA.

AC P01268;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Parathyroid hormone precursor (Parathyrin) (PTH).  
GN PTH.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=8005617; PubMed=388425;

RA Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,

RA Potts J.T., Jr., Rich A.;

RT "Cloning and nucleotide sequence of DNA coding for bovine  
preparathyroid hormone.";

RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).

[2]

RP SEQUENCE FROM N.A.

RX MEDLINE=82037785; PubMed=6170060;

RA Weaver C.A., Gordon D.F., Kemper B.;

RT "Introduction by molecular cloning of artifactual inverted sequences  
at the 5' terminus of the sense strand of bovine parathyroid hormone  
cDNA.";

RL Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).

[3]

RP SEQUENCE FROM N.A.

RX MEDLINE=83105964; PubMed=6185374;

RA Weaver C.A., Gordon D.F., Kemper B.;

RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";

RL Mol. Cell. Endocrinol. 28:411-424(1982).

[4]

RP SEQUENCE FROM N.A.

RX MEDLINE=84262483; PubMed=6086460;

RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;

RT "Isolation and complete nucleotide sequence of the gene for bovine  
parathyroid hormone.";

RL Gene 28:319-329(1984).

[5]

RP SEQUENCE OF 26-115.

RX MEDLINE=74142666; PubMed=4522780;

RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T., Jr.,

RA Cohn D.V.;

RT "The N-terminal amino-acid sequence of bovine preparathyroid  
hormone.";

```

RL Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE=71076162; PubMed=5531031;
RA Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
RA Aurbach G.D., Potts J.T. Jr.;
RT "The amino acid sequence of bovine parathyroid hormone I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE=71063634; PubMed=5275384;
RA Brewer H.B. Jr., Roman R.;
RT "Bovine parathyroid hormone: amino acid sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE=71091588; PubMed=4322265;
RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RA Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RT "Synthesis of a biologically active N-terminal tetraoctapeptide
RT of parathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN [9]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE=20090619; PubMed=10623601;
RA Marx U.C., Adernann K., Bayer P., Forssmann W.-G., Rosch P.;
RT "Solution structures of human parathyroid hormone fragments
RT hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
RT hPTH(1-37).";
RL Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL: V00106; CAA23439.1; -
DR EMBL: J00024; AAA30747.1; -
DR EMBL: K01938; AAA30749.1; -
DR EMBL: M25082; AAA30748.1; -
DR PIR: A01534; PTHO-.
DR PIR: A24949; A24949.
DR PDB: 1ZMC; 12-MAR-97.
DR InterPro: IPR001415; Parathyrd_hrm.
DR InterPro: IPR003625; Pthythorm_sub.
DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthythorm_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.
DR Hormone; Signal; 3d-structure.
KW SIGNAL
FT PROPEP 1 25
FT CHAIN 26 31
FT CHAIN 32 115
FT CHAIN 106 106
FT CHAIN 106 106
SQ SEQUENCE 115 AA; 12980 MW; 2ED246B34880710 CRC64;
Query Match 85.1%; Score 359; DB 1; Length 115;
Best Local Similarity 85.5%; Pred. No. 4.8e-33;
Matches 71; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 VSEIQLMHNIGKHLNEMEREWLRRKKLDVHNVALGAPLAPRDSQRPKRKEDNVLE 60
DB 33 VSEIQLMHNIGKHLNEMEREWLRRKKLDVHNVALGASLAVYDGSQRPKRKEDNVLE 92
QY 61 SHEKSLGEANKADYVNLTKAKSQ 83
DB 93 SHOKSLGEADKADYVNLTKAKPQ 115

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RESULT 5
PTHX_PIG STANDARD; PRT; 115 AA.
AC P01269;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN PTH.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
RT preproparathyroid hormone from pig and rat.";
RL Nucleic Acids Res. 15:6740-6740(1987).
RN [2]
RP SEQUENCE OF 26-115.
RX MEDLINE=76018954; PubMed=1164500;
RA Chu L.H., Huang W.-Y., Littlelike E.T., Hamilton J.W., Cohn D.V.;
RT "Porcine preparathyroid hormone. Identification, biosynthesis, and
RT partial amino acid sequence.";
RL Biochemistry 14:3631-3635(1975).
RN [3]
RP SEQUENCE OF 32-115.
RX MEDLINE=7425317; PubMed=4840833;
RA Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA Potts J.T. Jr.;
RT "The amino acid sequence of porcine parathyroid hormone.";
RL Biochemistry 13:1994-1999(1974).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL: X05722; CAA29193.1; -
DR PIR: A01535; PTHG.
DR PIR: B26806; B26806.
DR HSSP: P01270; 1BWV.
DR InterPro: IPR001415; Parathyrd_hrm.
DR InterPro: IPR003625; Pthythorm_sub.
DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthythorm_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.
DR Hormone; Signal.
KW SIGNAL
FT PROPEP 1 25
FT CHAIN 26 31
FT CHAIN 32 115
FT CHAIN 106 106
SQ SEQUENCE 115 AA; 12852 MW; 9FEBBCDE614BAC16 CRC64;
Query Match 84.1%; Score 355; DB 1; Length 115;
Best Local Similarity 84.3%; Pred. No. 1.3e-32;
Matches 70; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 VSEIQLMHNIGKHLNEMEREWLRRKKLDVHNVALGAPLAPRDSQRPKRKEDNVLE 60
DB 33 VSEIQLMHNIGKHLNEMEREWLRRKKLDVHNVALGASLVHNDGSQRPKRKEDNVLE 92
QY 61 SHEKSLGEANKADYVNLTKAKSQ 83

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Db      93 SHOKSLGSEADKAAVDVLIKAKPQ 115
      ||:|||||:|:|:| ||| |
RESULT 6
ID      PTHY_RAT          STANDARD:      PRT:      115 AA.
AC      P04089; 063473;
DT      01-NOV-1986 (Rel. 03, Last sequence update)
DT      01-NOV-1986 (Rel. 03, Last sequence update)
DE      Parathyroid hormone precursor (Parathyrin) (PTH).
GN      PTH.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=84135846; PubMed=6321505;
RA      Heinrich G., Kronenberg H.M., Potts J.T., Jr., Habener J.F.;
RT      "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
RT      gene and deduced amino acid sequence of rat preproparathyroid
RT      hormone."
RL      J. Biol. Chem. 259:3320-3329(1984).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87316938; PubMed=3628009;
RA      Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT      "Nucleotide sequence of a full-length cDNA clone encoding
RT      preproparathyroid hormone from pig and rat."
RL      Nucleic Acids Res. 15:6740-6740(1987).
RN      [3]
RP      SEQUENCE OF 10-115 FROM N.A.
RC      TISSUE=Parathyroid;
RA      Schmelzer H.-J., Gross G., Mayer H.;
RT      "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
RT      hormone."
RL      Adv. Gene Technol. 21:228-229(1984).
RN      [4]
RP      SEQUENCE OF 32-115 FROM N.A.
RC      STRAIN=Sprague-Dawley; TISSUE=Brain, Parathyroid, and Liver;
RX      MEDLINE=96079910; PubMed=7588314;
RA      Nucleic M.T., Parfitt S.A., Harvey S.;
RT      "Sequence analysis of hypothalamic parathyroid hormone messenger
RT      ribonucleic acid."
RL      Endocrinology 136:5600-5607(1995).
CC      -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC      BONE AND PREVENTING THEIR RENAL EXCRETION.
CC      -1- TISSUE SPECIFICITY: HYPOTHALAMUS AND PARATHYROID GLAND.
CC      -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; K01268; AAA41979.1; -
DR      EMBL; X05721; CA829192.1; -
DR      EMBL; M54875; AAA57156.1; -
DR      EMBL; S80127; -; NOT_ANNOTATED_CDS.
DR      PIR; A05091; A05091.
DR      PIR; A26806; A26806.
DR      HSSP; P01270; 1ZWB.
DR      InterPro: IPR001415; Parathyrd_hrm.
DR      InterPro: IPR003625; Pthythorm_sub.
DR      Pfam; PF01279; Parathyroid; 1.
DR      ProDom; PD010687; Pthythorm_sub; 1.
DR      SMART; SM00087; PTH; 1.
DR      PROSITE; PS00335; PARATHYROID; 1.

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KW      Hormone; Signal.
FT      SIGNAL 1 25
FT      PROPEP 26 31
FT      CHAIN 32 115
FT      CONFLICT 18 18 PARATHYROID HORMONE.
FT      CONFLICT 23 23 C -> Y (IN REF. 3).
FT      CONFLICT 33 33 A -> T (IN REF. 3).
FT      CONFLICT 33 33 V -> I (IN REF. 3).
FT      CONFLICT 62 62 V -> G (IN REF. 3).
SQ      SEQUENCE 115 AA; 12722 MW; 7B434CFCA528B230 CRC64;

Query Match 73.7%; Score 311; DB 1; Length 115;
Best Local Similarity 72.3%; Pred. No. 1e-27;
Matches 60; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY      1 VSEIQMLNHLGHLMSMEVEWLRKKLDVNFVALGAPLARDAGSQPRKEDNVLYE 60
      ||||||| ||||| :||:||||| ||||| :| : ||| |||:|||||
DB      33 VSEIQMLNHLGHLASVEWMLRRKKLDVNFVALGAPLARDAGSQPRKEDNVLYE 92
      ||||| :||||| |||||

QY      61 SHEKSLGSEANKADVNVLTFRKASQ 83
      : ||||| :||||| |||||
DB      93 GNSKSLGSECDKADVDVLYAKSQ 115

RESULT 7
ID      PTHY_CHICK          STANDARD:      PRT:      119 AA.
AC      P15743; 1
DT      01-APR-1990 (Rel. 14, Created)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      Parathyroid hormone precursor (PTH).
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89219100; PubMed=2710135;
RA      Russell J., Sherwood L.M.;
RT      "Nucleotide sequence of the DNA complementary to avian (chicken)
RT      preproparathyroid hormone mRNA and the deduced sequence of the
RT      hormone precursor."
RL      Mol. Endocrinol. 3:325-331(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89284968; PubMed=3251402;
RA      Khosla S., Demay M., Plines M., Hurwitz S., Potts J.T., Jr.,
RA      Kronenberg H.M.;
RT      "Nucleotide sequence of cloned cDNAs encoding chicken
RT      preproparathyroid hormone."
RL      J. Bone Miner. Res. 3:689-698(1988).
CC      -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC      BONE AND PREVENTING THEIR RENAL EXCRETION.
CC      -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC      -----
DR      EMBL; M31604; AAA49093.1; -
DR      EMBL; M36522; AAB02866.1; -
DR      PIR; A34937; A34937.
DR      HSSP; P01270; 1HPY.
DR      InterPro: IPR001415; Parathyrd_hrm.
DR      InterPro: IPR003625; Pthythorm_sub.
DR      Pfam; PF01279; Parathyroid; 1.
DR      ProDom; PD010687; Pthythorm_sub; 1.
DR      SMART; SM00087; PTH; 1.

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DR PROSITE: PS00335; PARATHYROID; 1.  
 KW Hormone; Signal.  
 FT SIGNAL 1 25  
 FT PROPEP 26 31  
 FT CHAIN 32 119 PARATHYROID HORMONE.  
 SQ SEQUENCE 119 AA: 13943 MW: B309D8E7729976E CRC64;  
 Query Match 41.4%; Score 174.5; DB 1; Length 119;  
 Best Local Similarity 44.7%; Pred. No. 1.4e-12;  
 Matches 42; Conservative 14; Mismatches 17; Indels 21; Gaps 2;  
 OY 1 VSFTLQMHNLGKHLNSMERVEMLRKKLDVHNFLALGAPLPADAGSORPRKKEDNVLE 60  
 DB 33 VSEQQLMHNLGHRHRTVERODWLOMKLDVHS-----ALEDAKTOPRPNKEDIVLGE 84  
 OY 61 -----SHEKSLGEANKADVNLTKAK 81  
 DB 85 IRRNRLLPEHLRAAVQKKSIDDKAYMNVLFKTK 118  
 RESULT 8  
 SYL\_THEME  
 ID SYL\_THEME STANDARD; PRT; 824 AA.  
 AC 09WV15;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Leucyl-tRNA synthetase (EC 6.1.1.4) (leucine--tRNA ligase) (leufs).  
 GN LEUS OR TM0168.  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;  
 OC Thermotogaceae; Thermotoga.  
 ON NCBI\_TaxID=2336;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MSB / DSM 3109;  
 RX MEDLINE=99287316; PubMed=10360571;  
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,  
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
 RA McDonald L., Ueberback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
 RT genome sequence of Thermotoga maritima."  
 RL Nature 399:323-329(1999).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.  
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 CC -----  
 DR EMBL: AE001702; AAD35261.1; -  
 DR TIGR: TM0168; -  
 DR InterPro: IPR002302; Leu-tRNA-synthla.  
 DR InterPro: IPR002300; tRNA-synt\_1a.  
 DR InterPro: IPR001412; tRNA-synt\_1.  
 DR Pfam: PF00133; tRNA-synt\_1; 1.  
 DR PRINTS: PR00985; TRNASYNTHLEU.  
 DR TIGRPFAM: TIGR00396; leus\_bact; 1.  
 DR PROSITE: PS00178; AA-trna\_ligase\_1; 1.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Complete proteome.  
 FT SITE 41 51 "HIGH" REGION.  
 FT SITE 580 584 "KMSK" REGION.  
 FT BINDING 583 583 ATP (BY SIMILARITY).

SQ SEQUENCE 824 AA: 95624 MW: 7CB0252A76A844EC CRC64;  
 Query Match 17.2%; Score 72.5; DB 1; Length 824;  
 Best Local Similarity 23.3%; Pred. No. 2.8;  
 Matches 21; Conservative 25; Mismatches 25; Indels 19; Gaps 4;  
 OY 4 IOLMHLGKHLNSMERVEMLRKKLDVHNFLALG-APLAP-----RDAGSORPRKKED 55  
 DB 692 MELVNLHLSQYLNLSVPOEWMNRKLLREIVEKTLALSPFAFLAEFPWHDGN-----D 744  
 OY 56 NVLVE-----SHEKSLGEANKADVNLTKAK 81  
 DB 745 SLVVQDSWPSYDPKALEVEVEETAIQINCK 774  
 RESULT 9  
 RBP1\_HUMAN  
 ID RBP1\_HUMAN STANDARD; PRT; 1257 AA.  
 AC P29374; Q15991; Q15992; Q15993;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Retinoblastoma-binding protein 1 (RBP1-1).  
 GN RBP1 OR RBP1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A. (ISOFORM I).  
 RX MEDLINE=94020841; PubMed=8414517;  
 RA Fattaei A.R., Helin K., Dembski M.S., Dyson N., Harlow E.,  
 RA Vuocolo G.A., Hanodik M.G., Haskell K.M., Olfiff A., Defeo-Jones D.,  
 RA Jones R.E.;  
 RT "Characterization of the retinoblastoma binding proteins RBP1 and  
 RT RBP2."  
 RL Oncogene 8:3149-3156(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND ALTERNATIVE SPLICING.  
 RX MEDLINE=93205410; PubMed=8455946;  
 RA Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.;  
 RT "Alternative splicing of the RBP1 gene clusters in an internal exon  
 RT that encodes potential phosphorylation sites."  
 RL Oncogene 8:949-957(1993).  
 RN [3]  
 RP SEQUENCE OF 855-1203 FROM N.A. (ISOFORM I).  
 RX MEDLINE=91312450; PubMed=1857421;  
 RA Defeo-Jones D., Huang P.S., Jones R.E., Haskell K.M., Vuocolo G.A.,  
 RA Hanodik M.G., Huber H.E., Olfiff A.,  
 RT "Cloning of cDNAs for cellular proteins that bind to the  
 RT retinoblastoma gene product."  
 RL Nature 352:251-254(1991).  
 CC -1- FUNCTION: INTERACTS WITH THE VIRAL PROTEIN-BINDING DOMAIN OF THE  
 CC RETINOBLASTOMA PROTEIN.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; I (shown here), II and III; are  
 CC produced by alternative splicing.  
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 CC -----  
 DR EMBL: S66427; AAB28543.1; -  
 DR EMBL: S57153; AAB25833.1; -  
 DR EMBL: S57160; AAB25834.1; -  
 DR EMBL: S57162; AAB25835.2; -  
 DR PIR: S16953; S16953.  
 DR Genew: HGNC:9885; RBP1.  
 DR MIM: 180201; -

DR InterPro: IPR001606; ARID.  
 DR InterPro: IPR000953; Chromo.  
 DR InterPro: IPR002999; Tudor.  
 DR Pfam: PF01388; ARID. 1.  
 DR SMART: SM00501; BRIGHT. 1.  
 DR SMART: SM00298; CHROMO. 1.  
 DR SMART: SM00333; TUDOR. 1.  
 DR Trans-acting factor; Nuclear protein; Alternative splicing.  
 FT DOMAIN 951 964  
 FT RETINOBLASTOMA PROTEIN BINDING  
 FT (POTENTIAL).  
 FT MISSING (IN ISOFORM I1).  
 FT VARSPLIC 1106 1174  
 FT VARSPLIC 1175 1175  
 FT VARSPLIC 1121 1174  
 FT VARSPLIC 1121 1174  
 FT CONFLICT 385 385  
 FT CONFLICT 618 618  
 FT CONFLICT 653 653  
 FT CONFLICT 779 779  
 FT CONFLICT 1178 1178  
 FT CONFLICT 1196 1201  
 FT CONFLICT 1257 AA; 142666 MW; F5C0ABD6D43DC CRC64;  
 SQ SEQUENCE

Query Match 17.1%; Score 72; DB 1; Length 1257;  
 Best Local Similarity 26.8%; Pred. No. 5.3;  
 Matches 19; Conservative 21; Mismatches 27; Indels 4; Gaps 2;

OY 13 HLNSMERVWLRRKLDVHN-EVALGAPLAPRAGSORPRKKEDNVLVESHEKSLGEANK 71  
 DB 1179 NNNSTRISFLQKLOEIRKYIWSLSEVATIDRRKRLLKKDREV---SHAGASSSAS 1235  
 OY 72 ADVNVLTFRKAS 82  
 DB 1236 SPTGNSPSSS 1246

RESULT 10  
 ID UL25\_HSV62 STANDARD; PRT; 555 AA.  
 AC P52537;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Virion protein US0.  
 GN US0 OR KALIR.  
 OS Human herpesvirus (type 6 / strain 229) (HHV6).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Roseolovirus.  
 OX NCBI\_TaxID=36351;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=95074921; PubMed=7983761;  
 RT Stanley F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.;  
 RT "Intragenomic linear amplification of human herpesvirus 68 orilyt  
 RT suggests acquisition of orilyt by transposition.";  
 RL J. VIROL. 69:589-596(1995).  
 CC -1- FUNCTION: VIRION PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,  
 CC EHV-1 36, EBV BVRFL, HCMV UL77, ILTV ORE2, AND VZV 34.  
 CC -----  
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 CC -----  
 CC EMBL; AF157706; AAB06348.1; -  
 CC InterPro: IPR002493; UL25.  
 DR Pfam: PF01499; UL25; 1.  
 DR SEQUENCE 555 AA; 63830 MW; 68B86590DC4CD2BC CRC64;  
 SQ

Query Match 16.5%; Score 69.5; DB 1; Length 555;  
 Best Local Similarity 35.4%; Pred. No. 3.8;

Matches 23; Conservative 10; Mismatches 27; Indels 5; Gaps 2;

OY 23 LRKKLDVHNFVALGAPLAPRAGSORPRKKEDNVLVESHEKSLGEA---NKADNVLT 78  
 DB 42 LRKKIDGHRDKLLRMLRKTDLALQKKQKSDVL-NSHLKAIEDLFTNDEGVNVEET 100  
 OY 79 KAKSQ 83  
 DB 101 KADTQ 105

RESULT 11  
 HSUL VIRCH STANDARD; PRT; 443 AA.  
 ID HSUL VIRCH  
 AC Q9KN07;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ATP-dependent hsl protease ATP-binding subunit hslU.  
 GN HSUL OR VC2674.  
 OS Vibrio cholerae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=666;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=El Tor N16961 / Serotype O1;  
 RX MEDLINE=20406833; PubMed=10952301;  
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Ginn M.L.,  
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 RA Fraser C.M.;  
 RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
 RA cholerae.";  
 RL Nature 406:477-483(2000).  
 CC -1- FUNCTION: CHAPERONE SUBUNIT OF A PROTEASOME-LIKE DEGRADATION  
 CC COMPLEX (BY SIMILARITY).  
 CC -1- SUBUNIT: INTERACTS WITH HSUL (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSUL SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AE004333; AAF95815.1; -  
 CC DR HSSP; P32168; IDO2.  
 DR TIGR; VC2674;  
 DR InterPro: IPR003959; AAA\_Arpase.  
 DR InterPro: IPR003959; AAA\_Arpase.  
 DR InterPro: IPR004491; HSP\_HsLVU.  
 DR Pfam: PF00004; AAA; 1.  
 DR SMART: SM00382; AAA; 1.  
 DR TIGRPFAM: TIGR00390; hslU; 1.  
 KW Chaperone; ATP-binding; Complete proteome.  
 FT NP\_BIND 57 64  
 FT ATP (POTENTIAL)  
 SQ SEQUENCE 443 AA; 49900 MW; DAEL3BE2FAB6A38F CRC64;

Query Match 15.9%; Score 67; DB 1; Length 443;  
 Best Local Similarity 28.8%; Pred. No. 5.6;  
 Matches 19; Conservative 16; Mismatches 27; Indels 4; Gaps 2;

OY 13 HLNSMERVWLRRKLDVHNFVALGAPLAPRAGSORPRKKEDNVLVESHEKSL--GEAN 70  
 DB 112 HQQAMKVKFRABEALAEVRLALPP--PRDAMGQAEQKENSSTROYFRKRLREGQLN 169  
 OY 71 KADVNV 76

Db 170 DKEIEI 175

# RESULT 12

UL25\_HSV6G STANDARD; PRT; 378 AA.

AC P52387; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Virion protein U50 (Fragment).

GN U50 OR LF3.

OS Human herpesvirus (type 6 / strain GS) (HHV6).

OC Betaherpesvirinae; Roseoloviridae;

OX NCBI\_TaxID=10369;

RN [1]

RP MEDLINE=91374623; PubMed=1654455;

RA Joseph S.F., Adlashi D.V., Salathuddin S.Z., Jagodzinski L.L., Wong-Staal F., Gallo R.C.;

RT "Identification of the human herpesvirus 6 glycoprotein H and putative large tegument protein genes.";

RT J. Virol. 65:5597-5604(1991).

CC -1- FUNCTION: VIRION PROTEIN.

CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25, EBV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.

CC -----

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CC -----

DR EMBL: S57509; AAB19777.1; -

DR InterPro: IPR002493; UL25.

DR Pfam: PF01499; UL25; 1.

FT NON\_TER 378 378

SO SEQUENCE 378 AA; 43459 MW; BE8B2EF416270AB6 CRC64;

Query Match 15.88; Score 66.5; DB 1; Length 378;

Best Local Similarity 33.88; Pred. No. 5.2;

Matches 22; Conservative 11; Mismatches 27; Indels 5; Gaps 2;

QY 23 LRKRLQDVHNFVALGAPLAPRDAGSOPRKEDVLVESHEKSUGEA-----NKADVNLVT 78

Db 42 LRKIDGHRKRLRMRLKLTETDLALQKKMKDSYVLSHLKATIEDALLFTNGEVNVT 100

QY 79 KAKSQ 83

Db 101 KADAQ 105

RESULT 13

UL25\_HSV6U STANDARD; PRT; 555 AA.

AC P52387; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Virion protein U50.

GN U50 OR BHRF3.

OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Betaherpesvirinae; Roseoloviridae;

OX NCBI\_TaxID=10370;

RN [1]

RP MEDLINE=95266321; PubMed=7747482;

RA Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,

Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,

Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,

Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,

Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,

Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,

Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,

Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,

Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,

Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,

Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,

RA Martin M.E., Estachiou S., Craxton M., Macaulay H.A.;

RT "The DNA sequence of human herpesvirus-6: structure, coding content, and genome evolution.";

RT Virology 209:29-51(1995).

RN [2]

RP SEQUENCE OF 1-378 FROM N.A.

RA MEDLINE=93091236; PubMed=133836;

RA Gompels U.A., Carrs A.L., Sun N., Arrand J.R.;

RT "Infectivity determinants encoded in a conserved gene block of human herpesvirus-6.";

RT DNA Seq. 3:25-39(1992).

CC -1- FUNCTION: VIRION PROTEIN.

CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25, EBV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.

CC -----

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CC -----

DR EMBL: X83413; CA58384.1; -

DR EMBL: X64320; CA45605.1; -

DR InterPro: IPR002493; UL25.

DR Pfam: PF01499; UL25; 1.

SO SEQUENCE 555 AA; 63594 MW; BA0C879FF56130D4 CRC64;

Query Match 15.88; Score 66.5; DB 1; Length 555;

Best Local Similarity 33.88; Pred. No. 8.2;

Matches 22; Conservative 11; Mismatches 27; Indels 5; Gaps 2;

QY 23 LRKRLQDVHNFVALGAPLAPRDAGSOPRKEDVLVESHEKSUGEA-----NKADVNLVT 78

Db 42 LRKIDGHRKRLRMRLKLTETDLALQKKMKDSYVLSHLKATIEDALLFTNGEVNVT 100

QY 79 KAKSQ 83

Db 101 KADAQ 105

RESULT 14

MIX1\_CAEL STANDARD; PRT; 1244 AA.

AC Q09591; 01-NOV-1997 (Rel. 35, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Mitotic chromosome and X-chromosome associated protein mix-1.

GN MIX-1 OR M106.1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;

OC Rhabditidae; Pelodermidae; Caenorhabditis.

OX NCBI\_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=98117254; PubMed=9458050;

RA Lieb J.D., Albrecht M.R., Chuang P.T., Meyer B.J.;

RT "MIX-1: an essential component of the C. elegans mitotic machinery executes X chromosome dosage compensation.";

RT Cell 92:265-277(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA STRAIN-Bristol N2;

RA Palmer S.;

RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Required for X-chromosome dosage compensation. Member of the dosage compensation complex that associates specifically with hermaphrodite X chromosomes to reduce their gene expression during interphase.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS



```

CC FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U96387; AAC47834.1; -
DR EMBL; Z46935; CAA87054.1; -
DR EMBL; AL031266; CAA20330.1; -
DR EMBL; Z46794; CAA20330.1; JOINED.
DR EMBL; Z46935; CAA20330.1; JOINED.
DR EMBL; Z46794; CAA86786.1; -
DR EMBL; AL031266; CAA86786.1; JOINED.
DR EMBL; Z46935; CAA86786.1; JOINED.
DR WormPep; M106.1; CEI8083.
DR InterPro; IPR003405; SMC_C.
DR InterPro; IPR003393; SMC_N.
DR Pfam; PF02483; SMC_N; 1.
DR ProDom; PD000006; ABC_transport; 1.
KW ATP-binding; Coiled coil; Nuclear protein.
FT NP_BIND 32 39 ATP (POTENTIAL).
FT DOMAIN 245 350 COILED COIL (POTENTIAL).
FT DOMAIN 415 479 COILED COIL (POTENTIAL).
FT DOMAIN 702 1043 COILED COIL (POTENTIAL).
FT DOMAIN 1109 1135 ALA/ASP-RICH (DA-BOX).
FT DOMAIN 1239 1242 POLY-ASP.
SQ SEQUENCE 1244 AA; 140341 MW; 255FD9C3D8C4AA49 CRC64;

Query Match 15.4%; Score 65; DB 1; Length 1244;
Best Local Similarity 26.8%; Pred. No. 31;
Matches 22; Conservative 16; Mismatches 34; Indels 10; Gaps 2;

QY 6 LMHNKGLKLNSEMER---VEMIRKRLQDVHNFVALGAPLRDAGSQRPRKEDNVLYES 61
DB 756 VVRDLKIVSEYEKNQAEIVTKLQVDEKIKTLESKMKDKNSQSRKKEITALLQK 815
QY 62 HE-----KSLGEANKADVNL 77
DB 816 AEOYVAQKNKNGEKARREVML 837

RESULT 15
KQUA.CHLPN STANDARD; PRT: 205 AA.
AC 092961;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylate kinase (EC 2.7.4.8) (GMP kinase).
GN GKM OR CP00120 OR CP0653.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CM1029;
RX MEDLINE=9920606; PubMed=10192388;
RA Kaiman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gall S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,

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RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shiral M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CML029 from USA."
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -1- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY, CGMP.
CC -1- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -1- SIMILARITY: BELONGS TO THE GUANYLATE KINASE FAMILY.
CC -----
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CC -----
DR EMBL; AE001598; AAD18273.1; -
DR EMBL; AE002223; AAF38466.1; -
DR EMBL; AP002545; BAA98331.1; -
DR HSSP; P15454; 1GKY.
DR PHC1-2DPAGE; Q92961; -.
DR TIGR; CP0653; -.
DR InterPro; IPR000619; Guanylate_kin.
DR Pfam; PF00623; Guanylate_kin; 1.
DR SMART; SM00072; Gukc; 1.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
KW Transferase; Kinase; ATP-binding; Complete proteome.
FT NP_BIND 26 33 ATP (BY SIMILARITY).
SQ SEQUENCE 205 AA; 23367 MW; 84A5422A624555F5 CRC64;

Query Match 15.3%; Score 64.5; DB 1; Length 205;
Best Local Similarity 26.1%; Pred. No. 43;
Matches 24; Conservative 21; Mismatches 30; Indels 17; Gaps 4;

QY 3 EIQLMHNKGLKLNSEMER---WLRKKLQDVHNFVA-----LGAPLR--DAGSORPR 51
DB 102 EIERIWSLCKHNAVYIDIGALFIRSMPSVFIAPPSQEBLERLARSGBESGRKE 161
QY 52 KQEDNVLESHEKSLGEANKADVNLTKAKSQ 83
DB 162 RLEHSLI-----ELAAANOQFYVILLDDLNQ 187

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Search completed: March 13, 2003, 15:00:50  
Job time : 12.291 secs

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 13, 2003, 14:57:54 ; Search time 32.209 Seconds  
(without alignments)  
530.968 Million cell updates/sec

Title: US-09-636-530-2

Perfect score: 422

Sequence: 1 VSEIQLMHNKGKHLNSMERY.....KSLGEANKADVNVLTAKSQ 83

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368	87.2	86	6 Q9N1V0	Q9N1V0 equus caball
2	358	84.8	115	6 Q9GL67	Q9GL67 felis silve
3	307	72.7	115	11 Q9Z0L6	Q9Z0L6 mus musculu
4	84	19.9	31	11 Q91Y91	Q91Y91 peromyscus
5	84	19.9	31	11 Q91Y90	Q91Y90 peromyscus
6	79.5	18.8	163	13 Q918E9	Q918E9 fugu rudrip
7	78.5	18.6	162	13 Q918U2	Q918U2 sparus aura
8	73	17.3	565	16 Q99WC5	Q99WC5 staphylococ
9	69	16.4	334	17 Q8TJX5	Q8TJX5 methanosarc
10	68.5	16.2	256	5 Q9VDC2	Q9VDC2 dtrosophila
11	68	16.1	607	16 Q8RG65	Q8RG65 fuscobacteri
12	67.5	16.0	1156	16 Q66878	Q66878 aquifex aeo
13	67	15.9	674	10 Q23544	Q23544 arabidopsis
14	66	15.6	215	5 Q17915	Q17915 caenorhabdi
15	66	15.6	341	17 Q97CE4	Q97CE4 thermoplasm
16	66	15.6	396	16 Q97MB3	Q97MB3 clostridium

17	66	15.6	886	10 Q8W3D7	Q8W3D7 oryza sativ
18	66	15.6	896	10 Q9SHT1	Q9SHT1 arabidopsis
19	66	15.6	1175	10 Q8S8B4	Q8S8B4 arabidopsis
20	65.5	15.5	861	10 Q9AVZ9	Q9AVZ9 guillardia
21	65	15.4	189	11 Q922S6	Q922S6 mus musculu
22	65	15.4	283	9 Q9AZW5	Q9AZW5 bacterioph
23	65	15.4	283	16 Q9CFN5	Q9CFN5 lactococcus
24	65	15.4	323	11 Q9CWX9	Q9CWX9 mus musculu
25	65	15.4	377	5 Q9XY80	Q9XY80 speleonecte
26	65	15.4	873	4 Q9NY03	Q9NY03 homo sapien
27	65	15.4	1226	4 Q9NZB6	Q9NZB6 homo sapien
28	65	15.4	1228	11 Q9JKB5	Q9JKB5 rattus norv
29	64.5	15.3	264	13 Q9SF76	Q9SF76 gallus gall
30	64.5	15.3	292	13 Q9PS77	Q9PS77 gallus gall
31	64.5	15.3	321	5 Q94940	Q94940 dtrosophila
32	64.5	15.3	495	4 Q9WUP4	Q9WUP4 homo sapien
33	64.5	15.3	668	6 Q9GLG4	Q9GLG4 sus scrofa
34	64.5	15.3	792	13 Q13110	Q13110 gallus gall
35	64.5	15.3	1018	3 Q9UST0	Q9UST0 schizosacch
36	64.5	15.3	1118	13 Q98951	Q98951 gallus gall
37	64.5	15.3	1137	13 Q93569	Q93569 gallus gall
38	64.5	15.3	1137	13 Q12942	Q12942 gallus gall
39	64	15.2	166	4 Q9UF62	Q9UF62 homo sapien
40	64	15.2	369	2 Q9F537	Q9F537 escherichia
41	64	15.2	459	4 Q9H915	Q9H915 homo sapien
42	64	15.2	667	17 Q8TIG5	Q8TIG5 methanosarc
43	64	15.2	784	4 Q9H5A0	Q9H5A0 homo sapien
44	64	15.2	1004	16 Q8XL47	Q8XL47 clostridium
45	63.5	15.0	376	11 Q99KR6	Q99KR6 mus musculu

## ALIGNMENTS

RESULT 1  
ID Q9N1V0 PRELIMINARY: PRT: 86 AA.

AC Q9N1V0:

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Parathyroid hormone (Fragment).

GN PTH.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI\_TaxID=9796;

RN [1]

RX MEDLINE=20082971; PubMed=10613847;

RA Caetano A.R., Shue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,

RA Bowling A.T., Murray J.D.;

RT "A comparative gene map of the horse (Equus caballus).";

RT Genome Res. 9:1239-1249(1999).

DR EMBL: AF134233; AAF62347.1; -

DR HSSP: P01270; 1HPY.

DR InterPro: IPR001415; Parathyrid\_hrm.

DR InterPro: IPR003625; Pthyrtorm\_sub.

DR Pfam: PF01279; Parathyroid.1.

DR ProDom: PD010687; Pthyrtorm\_sub.1.

DR SMART: SM00087; PTH.1.

DR PROSITE: PS00335; PARATHYROID.1.

FT NON\_TER

SO SEQUENCE

Query Match 87.2%; Score 368; DB 6; Length 86;  
Best Local Similarity 84.3%; Pred. No. 1.8e-33;  
Matches 70; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

OY 1 VSEIQLMHNKGKHLNSMERYEVLRRKLDVHNFFVALGAPLADAGSGRRPRKEDNVLE 60  
DB 4 VSEIQLMHNKGKHLNSMERYEVLRRKLDVHNFFVALGAPLADAGSGRRPRKEDNVLE 63

OY 61 SHEKSLGEANKADVNVLTKAKSQ 83  
 DB 64 SHOXSLGEADKADVNLTKAKSQ 86

## RESULT 2

O9GL67 PRELIMINARY: PRT: 115 AA.  
 AC O9GL67;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Preproparathyroid hormone precursor.  
 GN PTH.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;

RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;  
 RT "Molecular cloning of feline preproparathyroid hormone."  
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF309967; AAG30545.1; -.  
 DR HSSP; P01268; 1ZWC.  
 DR InterPro: IPR001415; Parathyrd\_hrm.  
 DR InterPro: IPR003625; Pthyrohm\_sub.  
 DR Pfam: PF01279; Parathyroid; 1.  
 DR ProDom: PD010687; Pthyrohm\_sub; 1.  
 DR SMART; SM00087; PTH; 1.  
 DR PROSITE; PS00335; PARATHYROID; 1.  
 GN Signal.  
 KW SIGNAL.  
 FT CHAIN 1 25 POTENTIAL.  
 FT SIGNAL 32 115 PARATHYROID HORMONE.  
 SQ SEQUENCE 115 AA: 12921 MW: 80CD557CC6A1A7E CRC64;

Query Match 84.8%; Score 358; DB 6; Length 115;  
 Best Local Similarity 83.1%; Pred. No. 3.3e-32;  
 Matches 69; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

OY 1 VSEIQLMHNLGKHLNEMEREMLRKLDVHNFGALPAPADAGSORPRKEDVAVE 60  
 DB 33 VSEIQLMHNLGKHLNEMEREMLRKLDVHNFGALPAPADAGSORPRKEDVAVE 92  
 OY 61 SHEKSLGEANKADVNVLTKAKSQ 83  
 DB 93 SHOXSLGEADKADVNLTKAKSQ 115

RESULT 3  
 O9ZOL6 PRELIMINARY: PRT: 115 AA.

AC O9ZOL6;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Parathyroid hormone precursor.  
 GN PTH.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

RN (1)  
 RP SEQUENCE FROM N.A.

RA Karaplis A.C., He B., Hlou-Tim F.F.T., Al-Akad B., Kronenberg H.M.;  
 RT "Cloning of the murine gene encoding parathyroid hormone: genomic  
 organization and nucleotide sequence."  
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF066075; AAC99656.1; -.  
 DR HSSP; P01270; 1ZWB.  
 DR MGD; MGI:97799; PTH.  
 DR InterPro: IPR001415; Parathyrd\_hrm.

DR InterPro: IPR003625; Pthyrohm\_sub.  
 DR Pfam: PF01279; Parathyroid; 1.  
 DR ProDom: PD010687; Pthyrohm\_sub; 1.  
 DR SMART; SM00087; PTH; 1.  
 DR PROSITE; PS00335; PARATHYROID; 1.  
 GN Signal.  
 KW SIGNAL.  
 FT CHAIN 1 25 POTENTIAL.  
 FT SIGNAL 32 115 PARATHYROID HORMONE.  
 SQ SEQUENCE 115 AA: 12825 MW: DAA3FABCB4E2FD9 CRC64;

Query Match 72.7%; Score 307; DB 11; Length 115;  
 Best Local Similarity 69.9%; Pred. No. 1.5e-26;  
 Matches 58; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

OY 1 VSEIQLMHNLGKHLNEMEREMLRKLDVHNFGALPAPADAGSORPRKEDVAVE 60  
 DB 33 VSEIQLMHNLGKHLNEMEREMLRKLDVHNFGALPAPADAGSORPRKEDVAVE 92  
 OY 61 SHEKSLGEANKADVNVLTKAKSQ 83  
 DB 93 SHOXSLGEADKADVNLTKAKSQ 115

RESULT 4  
 O91Y91 PRELIMINARY: PRT: 31 AA.

AC O91Y91;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Parathyroid hormone (Fragment).  
 GN PTH.  
 OS Peromyscus polionotus (Oldfield mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Peromyscus.  
 OX NCBI\_TaxID=42413;

RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Prince K.L., Dewey M.J.;  
 RT Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF382952; AAK63071.1; -.  
 DR InterPro: IPR001415; Parathyrd\_hrm.  
 DR InterPro: IPR003625; Pthyrohm\_sub.  
 DR Pfam: PF01279; Parathyroid; 1.  
 DR ProDom: PD010687; Pthyrohm\_sub; 1.  
 DR PROSITE; PS00335; PARATHYROID; UNKNOWN\_1.  
 GN NON\_TER 1 31  
 FT NON\_TER 31 31  
 SQ SEQUENCE 31 AA: 3461 MW: A208B0E772B9B55B CRC64;

Query Match 19.9%; Score 84; DB 11; Length 31;  
 Best Local Similarity 94.4%; Pred. No. 0.02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VSEIQLMHNLGKHLNEME 18  
 DB 14 VSEIQLMHNLGKHLNEME 31

RESULT 5  
 O91Y90 PRELIMINARY: PRT: 31 AA.

AC O91Y90;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE Parathyroid hormone (Fragment).  
 GN PTH.  
 OS Peromyscus maniculatus (Deer mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Peromyscus.





```
DR Pfam; PF02463; SMC_N_1.  
DR TIGRFAMs; TIGR00630; MG442_1.  
DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.  
KW Complete proteome.  
SQ SEQUENCE| 1156 AA; 135563 MW; B1ZDB30F7OCCE49 CRC64;  
  
Query Match. 16.0%; Score 67.5; DB 16; Length 1156;  
Best Local Similarity 29.0%; Pred. No. 96;  
Matches 27; Conservative 16; Mismatches 25; Indels 25; Gaps 4;  
  
QY 1 VSEIOLMHNLLCKHLSMSR-----VEMLRKKIDYHNHVALGAPLAPRDAGSORPR- 51  
DQ ||||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db 794 VSEIL-----KSLWEIERELNKKTYLEYLEKEIQEKER-----EREYLTERIKS 838  
  
QY 52 -KEDNVLVESHESKSLGEANKADYAVNLTKAKSQ 83  
DQ ||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db 839 LKKEIFENLIFREKTLQEVEKAEVAVNYVIYINRK 871  
  
RESULT 13  
O23544 PRELIMINARY; PRT; 674 AA.  
ID O23544 |  
AC O23544: 023543;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DE Hypothetical 75.3 kDa protein.  
GN ATG17000.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terry N.,  
RA Kreis M., Kavanagh T., Entian K.D., Kleger M., James R.,  
RA Puigdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A.,  
RA Jones J.F., Palme K., Ansong W., Delseny M., Bancroft I., Mewes H.W.,  
RA Schumacher C., Chalwatzis N.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; Z97342; CAB10480.1; -.  
DR EMBL; AL161545; CAB80971.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 674 AA; 75341 MW; F846AD8C3AC63C4 CRC64;  
  
Query Match. 15.9%; Score 67; DB 10; Length 674;  
Best Local Similarity 24.3%; Pred. No. 58;  
Matches 18; Conservative 21; Mismatches 31; Indels 2; Gaps 2;  
  
QY 12 KHLNSMER-VEMLRKKIDYHNHVALGAPLAPRDAGSORPRKK--EDNVLVESHESKSLG 67  
DQ |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db 271 KOIDDKDGVSITLKRRVKKEDPVPSSDPILKPYSNGMEVEDKTSRDPELLVENKSEELS 330  
  
QY 68 EANKADYAVNLTKAK 81  
DQ ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db 331 DTSKANNMNLOAR 344  
  
RESULT 14 |  
O17915 PRELIMINARY; PRT; 215 AA.  
ID O17915 |  
AC O17915: |  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE K01G5_4 protein.  
CN K01G5_4.  
GN Caenorhabditis elegans.
```

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxId=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wall M.;  
RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
investigating biology."  
RL Science 282:2012-2018(1998).  
CC -!- FUNCTION: GTP-BINDING PROTEIN INVOLVED IN NUCLEOCYTOPLASMIC  
TRANSPORT. REQUIRED FOR THE IMPORT OF PROTEIN INTO THE NUCLEUS AND  
ALSO FOR RNA EXPORT (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE RAN FAMILY IN THE RAS SUPERFAMILY.  
DR EMBL; 292803; CAB07240.1; -.  
DR HSPD; P17080; IRRP.  
DR InterPro; IPR002041; RAN.  
DR InterPro; IPR001806; Ras\_trnsfmg.  
DR InterPro; IPR005225; Small\_GTP.  
DR InterPro; IPR003575; Small\_GTPase.  
DR Pfam; PF00071; ras; 1.  
DR PRINTS; PR00627; GTPRANTC4.  
DR PRINTS; PR00449; RASTRNSFRMG.  
DR SMART; SM00176; RAN; 1.  
DR SMART; SM00010; small\_GTPase; 1.  
DR TIGRfams; TIGR00231; small\_GTP; 1.  
DR PROSITE; PS01115; RAN; 1.  
KW GTP-binding; Nuclear protein; Protein transport.  
SQ SEQUENCE 215 AA; 24254 MW; 90B32613588745E5 CRC64;

Query Match 15.6%; Score 66; DB 5; Length 215;  
Best Local Similarity 38.2%; Pred. No. 20;  
Matches 21; Conservative 7; Mismatches 17; Indels 10; Gaps 3;

OY 22 WLKKIQDVHN--FVALGAPLAPRDAGSORPRKKEDNVLESHEKSLGEANKADV 74  
DB 162 WLARKLGDPNLEFVAMPA-LAP-----PEYQMDPAMIAETEKDDNNAKADL 208

## RESULT 15

ID O97CE4 PRELIMINARY; PRT; 341 AA.  
AC O97CE4:  
DT 01-OCT-2001 (TREMBlrel. 18, Created)  
DT 01-OCT-2001 (TREMBlrel. 18, last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)  
DE Hypothetical protein TV0158.  
GN TV0158 OR TVG0169833.  
OS Thermoplasma volcanium.  
OC Archaea; Euryarchaeota; Thermoplasmatia; Thermoplasmales;  
OC Thermoplasmataceae; Thermoplasma.  
OX NCBI\_TaxId=50339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GSSI / DSM 4299 / JCM 9571;  
RX MEDLINE=20570466; PubMed=11121031;  
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,  
RA Kawashima T., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,  
RA Nunoshita T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.,  
RT "Archaeal adaptation to higher temperatures revealed by genomic  
sequence of Thermoplasma volcanium."  
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).  
DR EMBL; AP000991; BAB59300.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 341 AA; 38858 MW; D180D7AA274DC69 CRC64;

Query Match 15.6%; Score 66; DB 17; Length 341;  
Best Local Similarity 27.2%; Pred. No. 34;

Matches 22; Conservative 16; Mismatches 25; Indels 18; Gaps 5;  
OY 1 VSEIOLMNLGKHLNSMERVEWLRKKLQD--VHNFVALGAPLAPRDAGSORPRKKEDNVL 58  
DB 19 ISVETHTNLG--LNALF-VQLLRVNVDGNSAEFFAGL-----RRDVEDSTI 63  
OY 59 VESHEKSLGEANKADVNVLTG 79  
DB 64 IDVMROD-EGNYSVGYINTE 83

Search completed: March 13, 2003, 15:01:50  
Job time : 35.209 secs



GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: March 13, 2003, 14:48:44 ; Search time 176.53 Seconds  
(without alignments)  
303.138 Million cell updates/sec

Title: US-09-636-530-2

Perfect score: 422

Sequence: 1 VSEIQMLHNLGKHLNSMERV.....KSLGEANKADVNLTKAKSQ 83

## Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 64473110 residues

4569144

Total number of hits satisfying chosen parameters:

4569144

Minimum DB seq length: 0

0

Maximum DB seq length: 2000000000

2000000000

Post-processing: Minimum Match 0%

0%

Listing first 45 summaries

## Database :

Pending\_Patents\_AA\_Main:\*

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3: /cgn2\_6/ptodata/2/paa/US088.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US089.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US090.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/paa/US091.COMB.pep.\*  
7: /cgn2\_6/ptodata/2/paa/US092.COMB.pep.\*  
8: /cgn2\_6/ptodata/2/paa/US093.COMB.pep.\*  
9: /cgn2\_6/ptodata/2/paa/US094.COMB.pep.\*  
10: /cgn2\_6/ptodata/2/paa/US095.COMB.pep.\*  
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26: /cgn2\_6/ptodata/2/paa/US111.COMB.pep.\*  
27: /cgn2\_6/ptodata/2/paa/US112.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	422	100.0	83	US-09-636-530-2	Sequence 2, Appli
2	422	100.0	83	US-09-928-047B-1	Sequence 1, Appli
3	422	100.0	83	US-09-928-048A-4	Sequence 4, Appli
4	422	100.0	84	US-09-323-606C-1	Sequence 1, Appli
5	422	100.0	84	US-09-636-530-1	Sequence 1, Appli
6	422	100.0	84	US-09-928-047B-5	Sequence 5, Appli

	7	422	100.0	84	23	US-09-928-048A-3	Sequence 3, Appli
	8	418	99.1	82	17 <td>US-09-323-606C-2</td> <td>Sequence 2, Appli</td>	US-09-323-606C-2	Sequence 2, Appli
	9	418	99.1	82	20 <td>US-09-636-530-4</td> <td>Sequence 4, Appli</td>	US-09-636-530-4	Sequence 4, Appli
	10	418	99.1	82	23 <td>US-09-928-047B-2</td> <td>Sequence 2, Appli</td>	US-09-928-047B-2	Sequence 2, Appli
	11	417	98.8	83	24 <td>US-10-002-818-2</td> <td>Sequence 2, Appli</td>	US-10-002-818-2	Sequence 2, Appli
	12	417	98.8	84	1	PCR-US02-21356-1	Sequence 1, Appli
	13	417	98.8	84	3	PCR-US98-20848-1	Sequence 1, Appli
	14	417	98.8	84	3	US-07-806-271-2	Sequence 2, Appli
	15	417	98.8	84	4	US-08-016-171-2	Sequence 2, Appli
	16	417	98.8	84	7	US-08-329-856-2	Sequence 2, Appli
	17	417	98.8	84	7	US-08-345-151A-16	Sequence 16, Appli
	18	417	98.8	84	7	US-08-350-530A-25	Sequence 25, Appli
	19	417	98.8	84	7	US-08-350-709-9	Sequence 9, Appli
	20	417	98.8	84	7	US-08-350-709B-9	Sequence 9, Appli
	21	417	98.8	84	9	US-08-586-768-1	Sequence 1, Appli
	22	417	98.8	84	15	US-09-169-786-1	Sequence 1, Appli
	23	417	98.8	84	15	US-09-169-786-1	Sequence 1, Appli
	24	417	98.8	84	15	US-09-231-422B-2	Sequence 2, Appli
	25	417	98.8	84	16	US-09-231-422D-2	Sequence 2, Appli
	26	417	98.8	84	17	US-09-344-639D-1	Sequence 256, App
	27	417	98.8	84	20	US-09-657-276-256	Sequence 10, Appli
	28	417	98.8	84	22	US-09-843-221A-10	Sequence 1, Appli
	29	417	98.8	84	22	US-09-896-398-1	Sequence 1, Appli
	30	417	98.8	84	24	US-10-002-818-1	Sequence 1, Appli
	31	417	98.8	115	16	US-09-287-332-6	Sequence 6, Appli
	32	417	98.8	115	25	US-10-157-031-50	Sequence 50, Appli
	33	417	98.8	148	21	US-09-760-483-332	Sequence 332, App
	34	417	98.8	148	26	US-10-206-021-473	Sequence 473, App
	35	417	98.8	148	26	US-10-206-021-473	Sequence 332, App
	36	413	97.9	82	17	US-09-344-639D-2	Sequence 2, Appli
	37	412	97.6	84	1	PCR-US94-12205-1	Sequence 1, Appli
	38	412	97.6	84	8	US-08-455-919-1	Sequence 1, Appli
	39	412	97.6	84	8	US-08-458-075-1	Sequence 1, Appli
	40	410	97.2	84	8	US-08-466-487-16	Sequence 16, Appli
	41	409	96.9	80	17	US-09-323-606C-10	Sequence 10, Appli
	42	407	96.4	84	19	US-09-555-447-1	Sequence 1, Appli
	43	407	96.4	84	19	US-09-555-447-1	Sequence 1, Appli
	44	400	94.8	78	17	US-09-323-606C-4	Sequence 4, Appli
	45	400	94.8	78	23	US-09-928-047B-4	Sequence 4, Appli

## ALIGNMENTS

RESULT 1  
US-09-636-530-2  
; Sequence 2, Application US/09636530  
; GENERAL INFORMATION:  
; APPLICANT: Cantor, Thomas  
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR  
; FILE REFERENCE: 53421-2003.00  
; CURRENT APPLICATION NUMBER: US/09/636,530  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 83  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-636-530-2

Query Match 100.0%; Score 422; DB 20; Length 83;  
Best Local Similarity 100.0%; Pred. No. 1.6e-42;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VSEIQMLHNLGKHLNSMERVLRKKLODVHNFVALGAPLAPDAGSSORPKKEDVAVE	60
DB	1	VSEIQMLHNLGKHLNSMERVLRKKLODVHNFVALGAPLAPDAGSSORPKKEDVAVE	60
QY	61	SHEKSLGEANKADVNLTKAKSQ 83	
DB	61	SHEKSLGEANKADVNLTKAKSQ 83	

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RESULT 2
US-09-928-047B-1
; Sequence 1, Application US/09928047B
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITTING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20002.00
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-1

Query Match      100.0%; Score 422; DB 23; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.6e-42;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSEREWLRKKLDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
DB 1 VSEIQLMHNIGKHLNSEREWLRKKLDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
QY 61 SHEKSLGEANKADVNYLTAKSQ 83
DB 61 SHEKSLGEANKADVNYLTAKSQ 83

RESULT 3
US-09-928-048A-4
; Sequence 4, Application US/09928048A
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; FILE REFERENCE: 53221-20015.00
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-4

Query Match      100.0%; Score 422; DB 23; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.6e-42;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSEREWLRKKLDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
DB 1 VSEIQLMHNIGKHLNSEREWLRKKLDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
QY 61 SHEKSLGEANKADVNYLTAKSQ 83
DB 61 SHEKSLGEANKADVNYLTAKSQ 83

RESULT 4
US-09-323-606C-1
; Sequence 1, Application US/09323606C
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR

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; TITLE OF INVENTION: MODULATORS AND METHODS THEREFOR
; FILE REFERENCE: 53221-20009.00
; CURRENT APPLICATION NUMBER: US/09/323,606C
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-323-606C-1

Query Match      100.0%; Score 422; DB 17; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.6e-42;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSEREWLRKKLDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
DB 2 VSEIQLMHNIGKHLNSEREWLRKKLDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 61
QY 61 SHEKSLGEANKADVNYLTAKSQ 83
DB 62 SHEKSLGEANKADVNYLTAKSQ 84

RESULT 5
US-09-636-530-1
; Sequence 1, Application US/09636530
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
; FILE REFERENCE: 53221-20003.00
; CURRENT APPLICATION NUMBER: US/09/636,530
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-530-1

Query Match      100.0%; Score 422; DB 20; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.6e-42;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSEREWLRKKLDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
DB 2 VSEIQLMHNIGKHLNSEREWLRKKLDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 61
QY 61 SHEKSLGEANKADVNYLTAKSQ 83
DB 62 SHEKSLGEANKADVNYLTAKSQ 84

RESULT 6
US-09-928-047B-5
; Sequence 5, Application US/09928047B
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITTING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20002.00
; CURRENT FILING DATE: 2001-08-10
; CURRENT APPLICATION NUMBER: US/09/928,047B
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 84
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-928-047B-5

Query Match
Best Local Similarity 100.0%; Score 422; DB 23; Length 84;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIQLMHNIGKHLNSMERVEWMLRKKLQDVHNFVALGAPLAPRDAGSQRP RKKEDNVLYVE 60
DB 2 VSEIQLMHNIGKHLNSMERVEWMLRKKLQDVHNFVALGAPLAPRDAGSQRP RKKEDNVLYVE 61

OY 61 SHEKSLGEANKADVNVLTAKSQ 83
DB 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 7
US-09-928-048A-3
; Sequence 3, Application US/09928048A
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 3
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-3

Query Match
Best Local Similarity 100.0%; Score 422; DB 23; Length 84;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIQLMHNIGKHLNSMERVEWMLRKKLQDVHNFVALGAPLAPRDAGSQRP RKKEDNVLYVE 60
DB 2 VSEIQLMHNIGKHLNSMERVEWMLRKKLQDVHNFVALGAPLAPRDAGSQRP RKKEDNVLYVE 61

OY 61 SHEKSLGEANKADVNVLTAKSQ 83
DB 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 8
US-09-928-048C-2
; Sequence 2, Application US/09323606C
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
; FILE REFERENCE: 53221-20009.00
; CURRENT APPLICATION NUMBER: US/09/323,606C
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 2
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048C-2

Query Match
Best Local Similarity 99.1%; Score 418; DB 17; Length 82;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEIQLMHNIGKHLNSMERVEWMLRKKLQDVHNFVALGAPLAPRDAGSQRP RKKEDNVLYVE 61
DB 1 SEIQLMHNIGKHLNSMERVEWMLRKKLQDVHNFVALGAPLAPRDAGSQRP RKKEDNVLYVE 60
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OY 62 HEKSLGEANKADVNVLTAKSQ 83
DB 61 HEKSLGEANKADVNVLTAKSQ 82

RESULT 9
US-09-636-530-4
; Sequence 4, Application US/09636530
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS OR
; FILE REFERENCE: 53221-20003.00
; CURRENT APPLICATION NUMBER: US/09/636,530
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 4
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-530-4

Query Match
Best Local Similarity 99.1%; Score 418; DB 20; Length 82;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEIQLMHNIGKHLNSMERVEWMLRKKLQDVHNFVALGAPLAPRDAGSQRP RKKEDNVLYVE 61
DB 1 SEIQLMHNIGKHLNSMERVEWMLRKKLQDVHNFVALGAPLAPRDAGSQRP RKKEDNVLYVE 60

OY 62 HEKSLGEANKADVNVLTAKSQ 83
DB 61 HEKSLGEANKADVNVLTAKSQ 82

RESULT 10
US-09-928-047B-2
; Sequence 2, Application US/09928047B
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-2

Query Match
Best Local Similarity 100.0%; Score 418; DB 23; Length 82;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SEIQLMHNIGKHLNSMERVEWMLRKKLQDVHNFVALGAPLAPRDAGSQRP RKKEDNVLYVE 61
DB 1 SEIQLMHNIGKHLNSMERVEWMLRKKLQDVHNFVALGAPLAPRDAGSQRP RKKEDNVLYVE 60

OY 62 HEKSLGEANKADVNVLTAKSQ 83
DB 61 HEKSLGEANKADVNVLTAKSQ 82

RESULT 11
US-10-002-818-2
; Sequence 2, Application US/10002818
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; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyroid Hormone
; FILE REFERENCE: Renal Patients Having Secondary Hyperparathyroidism
; CURRENT APPLICATION NUMBER: US/10/002.818
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 2000 - ASCII format
; SEQ ID NO 2
; LENGTH: 83
; TYPE: PRF
; ORGANISM: human parathyroid hormone peptide fragment
US-10-002-818-2

Query Match          98.8%; Score 417; DB 24; Length 83;
Best Local Similarity 98.8%; Pred. No. 6.5e-42;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMEREWLRRKKLDQVHNFNVALGAPLAPRDAGSQRRPKKEDNVLYE 60
Db 1 VSEIQLMHNIGKHLNSMEREWLRRKKLDQVHNFNVALGAPLAPRDAGSQRRPKKEDNVLYE 60

QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
Db 61 SHEKSLGEANKADVNVLTKAKSQ 83

RESULT 12
PCT-US02-21356-1
; Sequence 1, Application PC/TUS0221356
; GENERAL INFORMATION:
; APPLICANT: Hutchinson, James Scott
; TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS
; FILE REFERENCE: A1713
; CURRENT APPLICATION NUMBER: PCT/US02/21356
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRF
; ORGANISM: Homo sapiens
PCT-US02-21356-1

Query Match          98.8%; Score 417; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 6.6e-42;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMEREWLRRKKLDQVHNFNVALGAPLAPRDAGSQRRPKKEDNVLYE 60
Db 2 VSEIQLMHNIGKHLNSMEREWLRRKKLDQVHNFNVALGAPLAPRDAGSQRRPKKEDNVLYE 61

QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
Db 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 13
PCT-US98-20848-1
; Sequence 1, Application PC/TUS9820848A
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: Method of Building and Maintaining Bone
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: PCT/US98/20848A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRF
; ORGANISM: Unknown
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; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Human
PCT-US98-20848-1

Query Match          98.8%; Score 417; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 6.6e-42;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMEREWLRRKKLDQVHNFNVALGAPLAPRDAGSQRRPKKEDNVLYE 60
Db 2 VSEIQLMHNIGKHLNSMEREWLRRKKLDQVHNFNVALGAPLAPRDAGSQRRPKKEDNVLYE 61

QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
Db 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 14
US-07-806-271-2
; Sequence 2, Application US/07806271
; GENERAL INFORMATION:
; APPLICANT: BOZZATO, Richard P.
; APPLICANT: KRONIS, K. Anne
; TITLE OF INVENTION: OXIDATION RESISTANT VARIANTS OF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Foley & Lardner
; STREET: 1800 diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/806,271
; FILING DATE: 19911213
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/156 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-806-271-2

Query Match          98.8%; Score 417; DB 3; Length 84;
Best Local Similarity 98.8%; Pred. No. 6.6e-42;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMEREWLRRKKLDQVHNFNVALGAPLAPRDAGSQRRPKKEDNVLYE 60
Db 2 VSEIQLMHNIGKHLNSMEREWLRRKKLDQVHNFNVALGAPLAPRDAGSQRRPKKEDNVLYE 61

QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
Db 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 15
US-08-016-171-2
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; Sequence 2, Application US/08016171  
; GENERAL INFORMATION:  
; APPLICANT: FUKUDA, Tsunehiko  
; APPLICANT: OSHIKA, Yuri  
; APPLICANT: YAMADA, Takao  
; TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN  
; TITLE OF INVENTION: PARATHYROID HORMONE  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/016,171  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/765,371  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILLIAMS, Gregory D  
; REGISTRATION NUMBER: 30,901  
; REFERENCE/DOCKET NUMBER: 41,288  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 84 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-016-171-2

Query Match 98.8%; Score 417; DB 4; Length 84;  
Best Local Similarity 98.8%; Pred. NO.6.6e-42;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIOLMHNIGKHLNMEVEWLRKKLDVHNFVALGAPLAPRDAGSQRRPKKEDNVIVE 60  
DB 2 VSEIOLMHNIGKHLNMEVEWLRKKLDVHNFVALGAPLAPRDAGSQRRPKKEDNVIVE 61  
QY 61 SHEKSLGEANKADVNVLTAKSQ 83  
DB 62 SHEKSLGEADKADVNVLTAKSQ 84

Search completed: March 13, 2003, 14:57:47  
Job time : 177.53 secs

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 13, 2003, 14:49:19 ; Search time 29.7313 Seconds  
(without alignments)  
362.927 Million cell updates/sec

Title: US-09-636-530-2

Perfect score: 422

Sequence: 1 VSEIQLMHNGKHLNSMERV.....KSLGEANKADVNLTKAKSQ 83

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 596842 seqs, 130003698 residues

Total number of hits satisfying chosen parameters: 596842

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/PCr\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	422	100.0	84	1	PCT-US02-25348-1
2	422	100.0	84	5	US-09-231-422F-2
3	422	100.0	84	6	US-10-215-770-1
4	417	98.8	84	1	PCT-US02-40891-505
5	417	98.8	84	1	PCT-US02-40891-508
6	417	98.8	84	1	PCT-US02-40891-531
7	417	98.8	84	1	PCT-US02-40891-531
8	417	98.8	84	1	PCT-US02-40891-532
9	417	98.8	84	1	PCT-US02-40891-626
10	417	98.8	84	5	PCT-US03-02155-13
11	417	98.8	84	5	US-09-383-550-1
12	417	98.8	84	6	US-10-224-522-1
13	417	98.8	84	6	US-10-311-366-10
14	417	98.8	692	1	PCT-US02-40891-289
15	417	98.8	692	1	PCT-US02-40891-292
16	417	98.8	693	1	PCT-US02-40891-314
17	417	98.8	693	1	PCT-US02-40891-315
18	417	98.8	693	1	PCT-US02-40891-316
19	417	98.8	693	1	PCT-US02-40891-410
20	400	94.8	78	5	US-09-231-422F-6
21	366	86.7	84	1	PCT-US02-25348-3
22	366	86.7	84	6	US-10-215-770-3
23	359	85.1	84	1	PCT-US02-25348-4
24	359	85.1	84	6	US-10-311-366-2
25	359	85.1	84	6	US-10-215-770-4
26	355	84.1	84	1	PCT-US02-25348-2

27	355	84.1	84	6	US-10-215-770-2	Sequence 2, Appli
28	315	74.6	84	6	US-10-311-366-11	Sequence 11, Appl
29	311	73.7	84	1	PCT-US02-25348-5	Sequence 5, Appli
30	311	73.7	84	6	US-10-215-770-5	Sequence 5, Appli
31	253	60.0	91	7	US-60-443-566-2959	Sequence 2959, Ap
32	253	60.0	123	7	US-60-443-566-2960	Sequence 2960, Ap
33	224	53.1	44	6	US-10-311-366-19	Sequence 19, Appl
34	193	45.7	38	6	US-10-311-366-18	Sequence 18, Appl
35	184.5	43.7	671	1	PCT-US02-40891-1199	Sequence 1199, Ap
36	184.5	43.7	671	1	PCT-US02-40891-1554	Sequence 1554, Ap
37	183	43.4	640	1	PCT-US02-40891-1580	Sequence 280, App
38	183	43.4	640	1	PCT-US02-40891-288	Sequence 288, App
39	183	43.4	640	1	PCT-US02-40891-1602	Sequence 1602, Ap
40	183	43.4	640	1	PCT-US02-40891-1603	Sequence 1603, Ap
41	183	43.4	643	1	PCT-US02-40891-241	Sequence 241, App
42	181.5	43.0	642	1	PCT-US02-40891-276	Sequence 276, App
43	178	42.2	643	1	PCT-US02-40891-267	Sequence 267, App
44	175	41.5	34	1	PCT-US02-40891-456	Sequence 456, App
45	175	41.5	34	1	PCT-US02-40891-457	Sequence 457, App

## ALIGNMENTS

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RESULT 1
PCT-US02-25348-1
; Sequence 1, Application PC/TUS0225348
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
; FILE OF INVENTION: THEREOF
; CURRENT APPLICATION NUMBER: PCT/US02/25348
; CURRENT FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-25348-1
Query Match      100.0%; Score 422; DB 1; Length 84;
Best Local Similarity 100.0%; Pred. No. 5.4e-40;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSEIQLMHNGKHLNSMERVLRKKLDVNFVALGAPLRDAGSQRRKEDNVLYE 60
DB 2 VSEIQLMHNGKHLNSMERVLRKKLDVNFVALGAPLRDAGSQRRKEDNVLYE 61
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
DB 62 SHEKSLGEANKADVNLTKAKSQ 84
RESULT 2
US-09-231-422F-2
; Sequence 2, Application US/09231422F
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas
; APPLICANT: Geo. Ping
; TITLE OF INVENTION: METHODS, KITS AND ANTIBODIES FOR DETECTING
; FILE OF INVENTION: PARATHYROID HORMONE
; CURRENT APPLICATION NUMBER: US/09/231,422F
; CURRENT FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens

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OY 61 SHEKSLGEADKADVNLTKAKSQ 83
|||||:|||||
DB 62 SHEKSLGEADKADVNLTKAKSQ 84

RESULT 6
PCT-US02-40891-530
; Sequence 530, Application PC/TUS0240891
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564PCT
; CURRENT APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 530
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-40891-530

Query Match 98.8%; Score 417; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 2e-39;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIOLMNLGKHLNMEVEWLRKKLDVHNFVALGAPLAPRDAGSORPRKKEDNVLYE 60
|||||:|||||
DB 2 VSEIOLMNLGKHLNMEVEWLRKKLDVHNFVALGAPLAPRDAGSORPRKKEDNVLYE 61

OY 61 SHEKSLGEADKADVNLTKAKSQ 83
|||||:|||||
DB 62 SHEKSLGEADKADVNLTKAKSQ 84

RESULT 7
PCT-US02-40891-531
; Sequence 531, Application PC/TUS0240891
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564PCT
; CURRENT APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
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; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 531
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-40891-531

Query Match 98.8%; Score 417; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 2e-39;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIOLMNLGKHLNMEVEWLRKKLDVHNFVALGAPLAPRDAGSORPRKKEDNVLYE 60
|||||:|||||
DB 2 VSEIOLMNLGKHLNMEVEWLRKKLDVHNFVALGAPLAPRDAGSORPRKKEDNVLYE 61

OY 61 SHEKSLGEADKADVNLTKAKSQ 83
|||||:|||||
DB 62 SHEKSLGEADKADVNLTKAKSQ 84

RESULT 8
PCT-US02-40891-532
; Sequence 532, Application PC/TUS0240891
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564PCT
; CURRENT APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 532
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-40891-532
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Query Match          98.8%; Score 417; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 2e-39;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNHGKHLNSMEREWMLRKKLQDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
Db 2 VSEIQLMHNHGKHLNSMEREWMLRKKLQDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 61

QY 61 SHEKSLGEADKADYVNLTKAKSQ 83
Db 62 SHEKSLGEADKADYVNLTKAKSQ 84

RESULT 9
PCT-US02-40891-626
; Sequence 626, Application PC/TUS0240891
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564PCT
; CURRENT APPLICATION NUMBER: PCT/US02/40891
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 626
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-40891-626

Query Match          98.8%; Score 417; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 2e-39;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNHGKHLNSMEREWMLRKKLQDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
Db 2 VSEIQLMHNHGKHLNSMEREWMLRKKLQDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 61

QY 61 SHEKSLGEADKADYVNLTKAKSQ 83
Db 62 SHEKSLGEADKADYVNLTKAKSQ 84

RESULT 10
PCT-US03-02155-13
; Sequence 13, Application PC/TUS0302155
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Potts, John T.
; TITLE OF INVENTION: Conformationally Constrained Parathyroid Hormone (PTH) Analogs
; TITLE OF INVENTION: With Lactam Bridges
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; FILE REFERENCE: 0609.514PC00
; CURRENT APPLICATION NUMBER: PCT/US03/02155
; CURRENT FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentln Version 3.2
; SEQ ID NO 13
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (84)..(84)
; OTHER INFORMATION: AMIDATION
PCT-US03-02155-13

Query Match          98.8%; Score 417; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 2e-39;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNHGKHLNSMEREWMLRKKLQDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
Db 2 VSEIQLMHNHGKHLNSMEREWMLRKKLQDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 61

QY 61 SHEKSLGEADKADYVNLTKAKSQ 83
Db 62 SHEKSLGEADKADYVNLTKAKSQ 84

RESULT 11
US-09-383-590-1
; Sequence 1, Application US/09383590
; GENERAL INFORMATION:
; APPLICANT: Backstrom, Kjell G. E.
; APPLICANT: Wallmark, Bjorn
; APPLICANT: Dahlback, Magnus
; APPLICANT: Edman, Peter
; APPLICANT: Johansson, Ann
; TITLE OF INVENTION: THERAPEUTIC PREPARATIONS FOR INHALATION
; FILE REFERENCE: 06275-110002
; CURRENT APPLICATION NUMBER: US/09/383,590
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 08/586,768
; PRIOR FILING DATE: 1996-01-30
; PRIOR APPLICATION NUMBER: PCT/SE95/01475
; PRIOR FILING DATE: 1995-12-08
; PRIOR APPLICATION NUMBER: SE 9404449-2
; PRIOR FILING DATE: 1994-12-22
; PRIOR APPLICATION NUMBER: SE 9502576-3
; PRIOR FILING DATE: 1995-07-12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-590-1

Query Match          98.8%; Score 417; DB 5; Length 84;
Best Local Similarity 98.8%; Pred. No. 2e-39;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNHGKHLNSMEREWMLRKKLQDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 60
Db 2 VSEIQLMHNHGKHLNSMEREWMLRKKLQDVHNFVALGAPLAPRDAGSQRRPKKEDNVLYE 61

QY 61 SHEKSLGEADKADYVNLTKAKSQ 83
Db 62 SHEKSLGEADKADYVNLTKAKSQ 84

RESULT 12
US-10-224-522-1
; Sequence 1, Application US/10224522
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GENERAL INFORMATION:  
APPLICANT: Backstrom, Kjell G. E.  
APPLICANT: Wallmark, Bjorn  
APPLICANT: Dahlbeck, Magnus  
APPLICANT: Edman, Peter  
APPLICANT: Johansson, Ann  
TITLE OF INVENTION: THERAPEUTIC PREPARATIONS FOR INHALATION  
FILE REFERENCE: 06275-110003  
CURRENT APPLICATION NUMBER: US/10/224,522  
CURRENT FILING DATE: 2002-08-19  
PRIOR APPLICATION NUMBER: US 09/383,590  
PRIOR FILING DATE: 1999-08-26  
PRIOR APPLICATION NUMBER: US 08/586,768  
PRIOR FILING DATE: 1996-01-30  
PRIOR APPLICATION NUMBER: PCT/SE95/01475  
PRIOR FILING DATE: 1995-12-08  
PRIOR APPLICATION NUMBER: SE 9404449-2  
PRIOR FILING DATE: 1994-12-22  
PRIOR APPLICATION NUMBER: SE 9502576-3  
PRIOR FILING DATE: 1995-07-12  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 84  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-224-522-1

Query Match 98.8%; Score 417; DB 6; Length 84;  
Best Local Similarity 98.8%; Pred. No. 2e-39;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIOLMHNLCGHLNSMERVEMLRKKLDVHNFVALGAPLAPRDAGSORPRKKEDNVAVE 60  
DB 2 VSEIOLMHNLCGHLNSMERVEMLRKKLDVHNFVALGAPLAPRDAGSORPRKKEDNVAVE 61  
OY 61 SHEKSLGEANKADYVNLTKAKSQ 83  
DB 62 SHEKSLGEADKADYVNLTKAKSQ 84

RESULT 13  
US-10-311-366-10  
Sequence 10, Application US/10311366  
GENERAL INFORMATION:  
APPLICANT: Holick, Michael F.  
TITLE OF INVENTION: Regulation Of Cell Proliferation And Differentiation Using Topical  
FILE REFERENCE: 1539, 0310001  
CURRENT APPLICATION NUMBER: US/10/311,366  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: PCT/US01/19650  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: US 60/213,247  
PRIOR FILING DATE: 2000-06-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 84  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: hPTH  
US-10-311-366-10

Query Match 98.8%; Score 417; DB 6; Length 84;  
Best Local Similarity 98.8%; Pred. No. 2e-39;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 61 SHEKSLGEANKADYVNLTKAKSQ 83  
DB 62 SHEKSLGEADKADYVNLTKAKSQ 84

RESULT 14  
PCT-US02-40891-289

Sequence 289, Application PCT/US0240891  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Albumin Fusion Proteins  
FILE REFERENCE: PF564PCT  
CURRENT APPLICATION NUMBER: PCT/US02/40891  
CURRENT FILING DATE: 2002-12-23  
PRIOR APPLICATION NUMBER: 60/341,811  
PRIOR FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/360,000  
PRIOR FILING DATE: 2002-02-28  
PRIOR APPLICATION NUMBER: 60/378,950  
PRIOR FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: 60/398,008  
PRIOR FILING DATE: 2002-07-24  
PRIOR APPLICATION NUMBER: 60/411,355  
PRIOR FILING DATE: 2002-09-18  
PRIOR APPLICATION NUMBER: 60/414,984  
PRIOR FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: 60/417,611  
PRIOR FILING DATE: 2002-10-11  
PRIOR APPLICATION NUMBER: 60/420,246  
PRIOR FILING DATE: 2002-10-23  
PRIOR APPLICATION NUMBER: 60/423,623  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/351,360  
PRIOR FILING DATE: 2002-01-28  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2222  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 289  
LENGTH: 692  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (532)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
PCT-US02-40891-289

Query Match 98.8%; Score 417; DB 1; Length 692;  
Best Local Similarity 98.8%; Pred. No. 2.5e-38;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIOLMHNLCGHLNSMERVEMLRKKLDVHNFVALGAPLAPRDAGSORPRKKEDNVAVE 60  
DB 610 VSEIOLMHNLCGHLNSMERVEMLRKKLDVHNFVALGAPLAPRDAGSORPRKKEDNVAVE 669  
OY 61 SHEKSLGEANKADYVNLTKAKSQ 83  
DB 670 SHEKSLGEADKADYVNLTKAKSQ 692

RESULT 15  
PCT-US02-40891-292  
Sequence 292, Application PCT/US0240891  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Albumin Fusion Proteins  
FILE REFERENCE: PF564PCT  
CURRENT APPLICATION NUMBER: PCT/US02/40891  
CURRENT FILING DATE: 2002-12-23  
PRIOR APPLICATION NUMBER: 60/341,811  
PRIOR FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/360,000

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; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 292
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-40891-292

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Query Match          98.8%; Score 417; DB 1; Length 692;
Best Local Similarity 98.8%; Pred. No. 2.5e-38;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQMHNIGKHLNMEVEVLRKKLDVYHNFVALGAPLAPRDAGSORPRKKEDNVLYE 60
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Db 23 VSEIQMHNIGKHLNMEVEVLRKKLDVYHNFVALGAPLAPRDAGSORPRKKEDNVLYE 82
    |||||||

QY 61 SHEKSLGEANKADVNVLTAKKASQ 83
    |||||||
Db 83 SHEKSLGEANKADVNVLTAKKASQ 105
    |||||||

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Search completed: March 13, 2003, 14:58:43  
 Job time : 30.7313 secs